

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 00:51:02 ; Search time 3003 seconds

(without alignments)
1952.014 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154
Sequence: 1 cggccgagctgctcattc.....gagatgacacgctccgagcg 154Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 3966416

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hcc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gsest1: *
9: gb_gsest2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.6	23.8	175	4	BF945949 CM0-NN115
2	36.6	23.8	175	4	BF945949 CM0-NN115
3	32.6	21.2	186	2	BF408161 UI-R-BJ2-
4	32.6	21.2	186	2	BF408161 UI-R-BJ2-
5	31.8	20.6	127	1	AA429110 zv78c11.r
6	31.8	20.6	127	1	AA429110 zv78c11.r
7	31.2	20.3	152	9	CL176108 104_382.1
8	31.2	20.3	152	9	CL176108 104_382.1
9	31.2	20.3	152	9	CL176109 104_382.1
10	31.2	20.3	152	9	CL176109 104_382.1
11	31.2	20.1	135	7	CV406622 RCO-TN007
12	31.2	20.1	135	7	CV406622 RCO-TN007
13	30.6	19.9	168	8	BH224923 1006122E0
14	30.6	19.9	168	8	BH224923 1006122E0
15	28.8	18.7	151	4	BI966631 id57a04.x
16	28.8	18.7	151	4	BI966631 id57a04.x
17	28.8	18.7	151	4	BI966631 id57a04.x
18	28.8	18.7	151	4	BI966631 id57a04.x
19	28.8	18.7	151	4	BI966631 id57a04.x
20	28.8	18.7	151	4	BI966631 id57a04.x
21	28.8	18.7	151	4	BI966631 id57a04.x
22	28.8	18.7	151	4	BI966631 id57a04.x
23	28.6	18.6	179	9	CE208692 tigr-gss-
24	28.6	18.6	179	9	CE208692 tigr-gss-

25	28.6	18.6	190	6	CA004311 HS17D13r
26	28.6	18.6	190	6	CA004311 HS17D13r
27	28.2	18.3	147	7	CN423515
28	28.2	18.3	147	7	CN423515
29	28.2	18.3	147	7	CN423515
30	28.2	18.3	147	7	CN423515
31	28.2	18.3	147	7	CN423515
32	28.2	18.3	147	7	CN423515
33	28.2	18.3	147	7	CN423515
34	28.2	18.3	147	7	CN423515
35	28.2	18.3	147	7	CN423515
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37	27.8	18.1	110	6	CB251950
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45	27.8	18.1	110	6	CB251950
46	27.8	18.1	110	6	CB251950
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50	27.8	18.1	110	6	CB251950
51	27.8	18.1	110	6	CB251950
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54	27.8	18.1	110	6	CB251950
55	27.8	18.1	110	6	CB251950
56	27.8	18.1	110	6	CB251950
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58	27.8	18.1	110	6	CB251950
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75	27.8	18.1	110	6	CB251950
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77	27.8	18.1	110	6	CB251950
78	27.8	18.1	110	6	CB251950
79	27.8	18.1	110	6	CB251950
80	27.8	18.1	110	6	CB251950
81	27.8	18.1	110	6	CB251950
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85	27.8	18.1	110	6	CB251950
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93	27.8	18.1	110	6	CB251950
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95	27.8	18.1	110	6	CB251950
96	27.8	18.1	110	6	CB251950
97	27.8	18.1	110	6	CB251950

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 99 26.4 17.1 182 7 C0504865 GGEZCB100
 c 100 26.4 17.1 182 7 C0504865 GGEZCB100

ALIGNMENTS

RESULT 1

BP945949 175 bp mRNA linear EST 22-JAN-2001
 LOCUS CMO-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BP945949
 ACCESSION BP945949
 VERSION BP945949.1 GI:12363224
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 175)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM0&t2=CM0-NN1155-
 271000-628-a09&t3=2000-10-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 175.
 Location/Qualifiers

FEATURES

source

1..175
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_id="NN1155"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 23.8%; Score 36.6; DB 4; Length 175;
 Best Local Similarity 65.1%; Pred. No. 32;
 Matches 54; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 70 GTCCGCGCCGCGCCGCTGACGATGAGCGAGATGACGCTCCGCGCCGCGCTGACGA 129
 Db 7 GTCTGTGCGGTAGGCTGAGGTGTGAGGAAAGACCACTCGGCGGTAGGCTGGGTGG 66
 QY 130 TGAGCGAGATGACGACGCTCCGCGC 152
 Db 67 TGAGAGAAATGACCACTCGCGGC 89

RESULT 2

BP945949/c 175 bp mRNA linear EST 22-JAN-2001
 LOCUS CMO-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BP945949
 ACCESSION BP945949
 VERSION BP945949.1 GI:12363224
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE

1 (bases 1 to 175)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800

COMMENT

Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM0&t2=CM0-NN1155-
 271000-628-a09&t3=2000-10-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 175.
 Location/Qualifiers

FEATURES

source

1..175
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_id="NN1155"
 /note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
 Site_2: SmaI; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 23.8%; Score 36.6; DB 4; Length 175;
 Best Local Similarity 65.1%; Pred. No. 32;
 Matches 54; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 QY 3 GCCGAGCTGCTCATCTCGCTCATCTCGATGCGCGCGCGAGCTGTCATCTCGCTCA 62
 Db 89 GCCGAGCTGCTCATCTCTCTCAACACCGCTACCGCCGACGTCGCTTCCCTCA 30
 QY 63 TCGTCAGTCGCGCGCGCGCGAC 85
 Db 29 CCACCCAGCTACCGCGCACAGAC 7
 RESULT 3
 BP408161 186 bp mRNA linear EST 28-NOV-2000
 LOCUS UI-R-BJ2-bra-d-05-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
 DEFINITION

ACCESSION UI-R-BJ2-bra-d-05-0-UI 3', mRNA sequence.
 VERSION BF408161
 KEYWORDS
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 EST.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Rattus.
 1 (bases 1 to 186)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Oligo-dT track not found, Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 1-21,
 >CC_rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source
 Location/Qualifiers
 1..186
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BJ2-bra-d-05-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="UI-R-BJ2"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-BJ2
 library is a subtracted library derived from the following
 tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
 atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
 dpc, AV canal at 15 dpc. For a detailed description of
 the library from which this clone was derived, please
 visit our web site at ratest.eng.uiowa.edu. The
 subtraction has been previously described in (Bonaldo,
 Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"

ORIGIN
 Query Match 21.2%; Score 32.6; DB 2; Length 186;
 Best Local Similarity 54.6%; Pred. No. 3.2e+02;
 Matches 65; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 Oy 35 CGCGCGCGGAGCTGTCATCTGCTCATCTGCGTGGCGCGCGGACTCGAGTATG 94
 Db 17 CGGCGCTCTGGCATGGGCGCGGCGGATGATGTCTAGTCGCGCGCTGGCGACCGGG 76
 Oy 95 AGCGAGATGACAGCTCCGCGCGCGGACTCGACGATGAGGAGATGACAGCTCCGGCC 153
 Db 77 AGCGGAGGCTGGGCTTCGCGCTCCGATGACATGAAGTGTGGCTGAGAGCCCCCCCC 135

RESULT 4
 LOCUS BF408161 186 bp mRNA linear EST 28-NOV-2000
 DEFINITION UI-R-BJ2-bra-d-05-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
 ACCESSION BF408161
 VERSION BF408161.1 GI:11396136

KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 Rattus.
 1 (bases 1 to 186)
 Bonaldo,M.F., Lennon,G. and Soares,M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548
 COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Oligo-dT track not found, Not 1 site shown in beginning of sequence
 is likely internal to the message. cDNA Library Preparation: M.B.
 Soares Lab Clone distribution: clones will be available through
 Research Genetics (www.resgen.com) The following repetitive
 elements were found in this cDNA sequence: 1-21,
 >CC_rich#low_complexity
 Seq primer: M13 Forward
 POLYA-No.

FEATURES
 source
 Location/Qualifiers
 1..186
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-BJ2-bra-d-05-0-UI"
 /lab_host="DH10B (Life Technologies)"
 /clone_id="UI-R-BJ2"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site 1: Not 1; Site 2: Eco RI; The UI-R-BJ2
 library is a subtracted library derived from the following
 tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
 atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
 dpc, AV canal at 15 dpc. For a detailed description of
 the library from which this clone was derived, please
 visit our web site at ratest.eng.uiowa.edu. The
 subtraction has been previously described in (Bonaldo,
 Lennon and Soares, Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"

ORIGIN
 Query Match 21.2%; Score 32.6; DB 2; Length 186;
 Best Local Similarity 54.6%; Pred. No. 3.2e+02;
 Matches 65; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
 Oy 2 GCGCGAGCTGTCATCTGCTCATCTGCGTGGCGCGGAGCTGTCATCTGCTC 61
 Db 135 GGGGGGGGGCTCCAGCCCACTTATGATCGGAGCCGAGGCCAGCTCCGCTC 76
 Oy 62 ATGTCGATGCGGCGCGCGGACTCGACGATGAGGAGATGACCAAGCTCCGCGCG 120
 Db 75 CCGGCGTCCGCGGCGGCGGCGGAGTACACTATCCCGCGCCAGCCAGAGGCG 17

RESULT 5
 LOCUS AA429110 127 bp mRNA linear EST 16-OCT-1997
 DEFINITION zv78c11.r1 Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone
 IMAGE:759764.5' similar to TR:G307305 G307309 HISTONE H4. [1] ;
 mRNA sequence.
 ACCESSION AA429110
 VERSION AA429110.1 GI:2110653
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 127)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,
White, Y., Wylie, T., Waterston, R. and Wilson, R.
TITLE Washu-Merck EST Project 1997
JOURNAL Unpublished (1997)
COMMENT Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 127
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:759764"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 20.6%; Score 31.8; DB 1; Length 127;
Best Local Similarity 61.4%; Pred. No. 5.1e+02;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 35 CGCGCGCGGAGCTGCTCATCTCGTCAATCGAGTCGGCGCGCGACTCGACGATG 94
DB 32 CGCGAGCGCGAGCTGCGAGCGAGCTCATCTCATGTCGACGCGCTCTCGGCTCG 91
QY 95 AGCGAGTACGACGAGCTCGCGCGG 117
DB 92 GAGGAGAGCCCAAGCCGAGCAG 114

RESULT 6
AA429110/c 127 bp mRNA linear EST 16-OCT-1997
LOCUS z478c11.r1 Soares total_fetus_Nb2H8 9w Homo sapiens cDNA clone
DEFINITION IMAGE:759764 5' similar to TR:G307309 G307309 HISTONE H4. [1] ;
mRNA sequence.
ACCESSION AA429110
VERSION AA429110.1 GI:2110653
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 127)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J.,
Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B.,

TITLE White, Y., Wylie, T., Waterston, R. and Wilson, R.
JOURNAL Washu-Merck EST Project 1997
COMMENT Unpublished (1997)
Contact: Wilson R.
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1. 127
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:759764"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCTTAATTTTCTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Query Match 20.6%; Score 31.8; DB 1; Length 127;
Best Local Similarity 61.4%; Pred. No. 5.1e+02;
Matches 51; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
QY 38 CGCGCGGAGCTGCTCATCTCGTCAATCGTCAATCGAGTCGGCGCGCGACTCGACGATG 97
DB 114 CTGTCGCGCTGTCGAGCGCTCTCTCCGAGCGCGAGAGCGCTGCGACGATGATGAGC 55
QY 98 GAGATGACGAGCTCGCGCGCGCG 120
DB 54 TCCTGTTCAGCTCGGCTTCGCG 32

RESULT 7
CL176108 152 bp DNA linear GSS 06-JUN-2004
LOCUS 104_382_10892902_116_31763_118 Sorghum methylation-filtered library
DEFINITION (LibID: 104) Sorghum bicolor genomic clone 10892902, genomic survey
sequence.
ACCESSION CL176108
VERSION CL176108.1 GI:40688623
KEYWORDS GSS.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 152)
AUTHORS Budiman, M.A., Flick, E., Jones, J., Nunberg, A., Citek, R.W.,
Robbins, D., Rohlfing, T., Bradford, K., Fries, J., McEnamy, J.,
Trani, L., Isak, A., Zimmerman, C., Lakey, N. and Bedell, J.A.
Genethresher methylation filtered genomic sequences from Sorghum
bicolor
JOURNAL Unpublished (2004)
COMMENT Contact: Bedell JA
Otion Genomics, LLC
4041 Forest Park Ave, St. Louis, MO 63108, USA

Query Match 20.3%; Score 31.2; DB 9; Length 152;
 Best Local Similarity 66.2%; Pred. No. 7.2e+02;
 Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 20 CGCTCATCTGAGTCGGCGCCGAGCTGTCATCTCGTCATCTGAGTCGAGTCGGCGCC 79
 Db 31 CCCCCAACCTCCAGCGCGCTGAGAGGGCTTCATCTGTCGCCCGCTACTCCGTCGCC 90

QY 80 GCCGACTC 87
 Db 91 GCCGACTC 98

RESULT 10
 CL176109/c 152 bp DNA linear GSS 06-JAN-2004
 LOCUS 104_332_10892902_148_31762_118 Sorghum methylation-filtered library
 DEFINITION (libID: 104) Sorghum bicolor genomic clone 10892902, genomic survey
 sequence.

ACCESSION CL176109
 VERSION CL176109
 KEYWORDS GSS.
 SOURCE CL176109.1 GI:40688624
 ORGANISM Sorghum bicolor (sorghum)
 Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Sorghum.
 1 (bases 1 to 152)
 Budiman,M.A., Flick,E., Jones,J., Nunberg,A., Citek,R.W.,
 Robbins,D., Rohlfing,T., Bradford,K., Fries,J., McMenamy,J.,
 Trani,L., Isak,A., Zimmerman,C., Lakey,N. and Bedell,J.A.
 GenetResher methylation filtered genomic sequences from Sorghum
 bicolor
 Unpublished (2004)
 Contact: Bedell JA
 Orion Genomics, LLC
 4041 Forest Park Ave, St. Louis, MO 63108, USA
 Tel: 314 615 6979
 Fax: 314 615 5975
 Email: jbedell@oriongenomics.com
 Plate: 382 row: e column: 22
 Seq primer: SWfor Forward
 Class: shotgun
 High quality sequence stop: 152.

FEATURES
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 location/Qualifiers
 1..152
 /organism="Sorghum bicolor"
 /mol_type="genomic DNA"
 /cultivar="ATx623"
 /db_xref="taxon:4558"
 /clone="10892902"
 /clone_lib="Sorghum methylation-filtered library (libID:
 104)"
 /note="Organ: leaf; Vector: pBCSK(-); Site: 1: HincII; DNA
 prepared from purified nuclei was randomly sheared,
 end-repaired, size fractionated to enrich for the 0.5 to 5
 kb fraction, ligated into HincII-digested pBCSK(-) vector
 and electroporated into E. coli cells. This is a
 methylation-filtered library."

ORIGIN
 Query Match 20.3%; Score 31.2; DB 9; Length 152;
 Best Local Similarity 66.2%; Pred. No. 7.2e+02;
 Matches 45; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 68 GAGTCGGCGCGCGCTCGACGATGACGATGACGACCTCCGCGCGGACCTCGAC 127
 Db 98 GAGTCGGCGCGCGGAGATGAGCGCGGAGCGAGATGAGCCCTCTCGACCGCGGTGAG 39

QY 128 GATGAGCG 135
 Db 38 GTTGGGGG 31

RESULT 11
 CV406622 135 bp mRNA linear EST 28-SEP-2004
 LOCUS RC0-TN0078-110700-031-f03 TN0078 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 CV406622
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 135)
 Dias Neto,E., Garcia Correa,R., Verjoveki-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 2020263
 MEDLINE
 PUBMED
 10737800
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. <http://www.ludwig.org.br>.
 Location/Qualifiers
 1..135
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="TN0078"
 /note="Organ: testis_normal; Vector: puc18; Site: 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 20.1%; Score 31; DB 7; Length 135;
 Best Local Similarity 62.0%; Pred. No. 8.1e+02;
 Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CGGCCGAGGTGTCATCTGCTCATCTGAGTCGCGCGCGAGCTGTCATCTGCT 60
 Db 57 CGCGCGAGCTGACTTCTCCCTACACCCAGCTTACCGCGAGCTGCTCTTCCCT 116

QY 61 CATTCTGAGTCGGCGGCC 79
 Db 117 CACCACCCAGACTACGACC 135

RESULT 12
 CV406622/c 135 bp mRNA linear EST 28-SEP-2004
 LOCUS RC0-TN0078-110700-031-f03 TN0078 Homo sapiens cDNA, mRNA sequence.
 DEFINITION
 CV406622
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

source

1. .168
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="mixed background #23/A186/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="1006 - RescueMu Grid G"
/note="Organ: leaf; Vector: RescueMu (engineered from pBluescript backbone); Site_1: BamHI, Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu'. Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 19.9%; Score 30.6; DB 8; Length 168;
Best Local Similarity 60.0%; Pred. No. 1e+03;
Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Oy 22 CTCATCTGAGTGGGCGCGGAGCTGATCTCGCTCATCTGCGAGTGGCGCGCC 81
Db 117 CTCCTCTGCGGGCTCGACGGCGCGCGAGCGCTGCTGCGGAGCGGCGCGCCAC 58
Oy 82 CGACTCGACGATGAGCGAGTACC 106
Db 57 CTGGCCGACGCGGAGCGTGAGCC 33

RESULT 15
BI966631 151 bp mRNA linear EST 12-MAR-2002
LOCUS i457a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
DEFINITION musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P94852
P11 PROTEIN. ; mRNA sequence.
BI966631
BI966631.1 GI:16341036
EST.
Mus musculus (house mouse)
ORIGIN Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@iobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
MG1:1953309 This sequence now available from the IMAGE consortium,

for clone orders contact: info@image.llnl.gov
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1. .151
/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5666983"
/sex="Both for embryonic & newborn, male for adult and adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
/lab_host="DH10B"
/clone_1lb="Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1"
/note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were separately constructed using SuperScript Plasmid Library Kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

ORIGIN

Query Match 18.7%; Score 28.8; DB 4; Length 151;
Best Local Similarity 60.0%; Pred. No. 2.8e+03;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Oy 40 GCCGAGCTGATCTGCTGCTCATCTGAGTGGCGCGCGACTCGACGATGACGA 99
Db 34 GCTGAGAGAGTCCGCGACGCGCTCGCGGAGTGGCGCTGACCGGCTGACCGA 93
Oy 100 GATGACCAAGCTCCGCGCGCC 119
Db 94 GGTCAAGGCTTCGCGCGCC 113

RESULT 16
BI966631 151 bp mRNA linear EST 12-MAR-2002
LOCUS i457a04.x1 Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus
DEFINITION musculus cDNA clone IMAGE:5666983 3' similar to TR:P94852 P94852
P11 PROTEIN. ; mRNA sequence.
BI966631
BI966631.1 GI:16341036
EST.
Mus musculus (house mouse)
ORIGIN Mus musculus
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 151)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvilli, R.,
Williams, T., Jackson, Y. and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@iohnp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
WGI:1953309 This sequence now available from the IMAGE consortium,
for clone orders contact: info@image.llnl.gov
High quality sequence stop: 1.

FEATURES

source

1.151
location/Qualifiers

/organism="Mus musculus"
/mol_type="mRNA"
/strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5666983"
/sex="Both for embryonic & newborn, male for adult and adult islet"
/dev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"
/lab_host="DH10B"
/clone_lib="Melton Normalized Mixed Mouse Pancreas 1 N1-MSI"
/note="Vector: pSPORT1, Site 1: Not I, Site 2: Sal I, Five libraries representing E10.5/12.5 pancreatic bud, E16.5 pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were separately constructed using Superscript plasmid library kit (Life Technologies). cDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806, 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an EcoT of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

ORIGIN

Query Match

Best Local Similarity 18.7%; Score 28.8; DB 4; Length 151;
Matches 48; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Qy 36 GCGCGCGGAGCTGCTCATCTGCTGAGTGGCGCGCGGCGGAGTCTGACGATGA 95
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Db 113 GCGCGCGGAGCTTACCTTACCTGCTGAGTGGCGCGCGGCGGAGTCTGCGGAGGG 54
|||||
Qy 96 GCGAGATGACGAGCTCCGCGC 115
|||||
Db 53 CCTCGCGGAGCTCTCTCGAGC 34
|||||

RESULT 17
CA002143 167 bp mRNA linear EST 23-OCT-2002
LOCUS HS06K10r HS Hordeum vulgare subsp. vulgare cDNA clone HS06K10
DEFINITION
ACCESSION CA002143
VERSION CA002143.1 GI:24279125
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 167)
Zhang, H., Potokina, E., Michalek, W., Weeschke, W., Stein, N. and

TITLE Graner, A.
JOURNAL Barley ESTs from germinating seeds
COMMENT Unpublished (2002)
Contact: Stein Nils

Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 167 Std Error: 0.00
Plate: 6 row: K column: 10
Seq primer: M13rev.

FEATURES

source

1.167
location/Qualifiers

/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="barke"
/sub_species="vulgare"
/db_xref="GABI:257345"
/db_xref="taxon:112509"
/clone="HS06K10"
/issue_type="embryo + scutellum"
/dev_stage="0-16 hours after imbibition"
/lab_host="XL10-Gold"
/clone_lib="HS"
/note="Vector: Bluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match

Best Local Similarity 18.7%; Score 28.8; DB 6; Length 167;
Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

Qy 56 TCGCTCATCTGCTGAGTGGCGCGCGCGGAGTCTGACGATGACGATGACGCTCCGCGC 115
|||||
Db 35 TCGCGCTCTCCGATGCGGCGCGCGCGCGCGCGGAGTGAAGATCGCGAGCGCGTC 94
|||||
Qy 116 GCGGACTCGACGATGACGATGACGATGACGATGACGATGACGATGACGATGAC 151
|||||
Db 95 AGATTCGCGCGCGGAGTCTGAGAGAGACGAGAGCGG 130
|||||

RESULT 18
CA002143/c 167 bp mRNA linear EST 23-OCT-2002
LOCUS HS06K10r HS Hordeum vulgare subsp. vulgare cDNA clone HS06K10
DEFINITION
ACCESSION CA002143
VERSION CA002143.1 GI:24279125
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 167)
Zhang, H., Potokina, E., Michalek, W., Weeschke, W., Stein, N. and Graner, A.
Barley ESTs from germinating seeds
JOURNAL Unpublished (2002)
CONTACT: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595

Email: stein@ipk-gatersleben.de
 Insert length: 167 Std Error: 0.00
 Plate: 6 row: K column: 10
 Seq primer: M13rev
 Location/Qualifiers

FEATURES

SOURCE

1. 167
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
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 /db_xref="GABI:257345"
 /db_xref="taxon:112509"
 /clone="HS06K10"
 /tissue_type="embryo + scutellum"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HS"
 /note="vector: pBluescript SK+; site_1: EcoRI (5'-end of cDNA); site_2: XhoI (3'-end of cDNA). Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable."

ORIGIN

Query Match 18.7%; Score 28.8; DB 6; Length 167;
 Best Local Similarity 56.2%; Pred. No. 2.8e+03;
 Matches 54; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 4 CCGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCCGAGCTGCTCATCTCGCTCAT 63
 DB 130 CCGCTCCGCTCTCTCTCAGCTCGTCGCCGCGATCTCGAGCGCTCTCTCTCTAC 71
 QY 64 CGTCGAGTCGGCGCGCCGCGACTCGACGATGAGCGA 99
 DB 70 CTCGCGCGCCGCGCGCCGCGACCGGAGAGGCCGCA 35

RESULT 19
 BF882476 184 bp mRNA linear EST 17-JAN-2001
 LOCUS BF882476
 DEFINITION CM1-ET0191-051200-626-b02 ET0191 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF882476
 VERSION BF882476.1 GI:12272602
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 184)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 180.
 Location/Qualifiers

FEATURES

SOURCE

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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="ET0191"
 /note="Organ: lung tumor; Vector: puc18; site_1: SmaI; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 18.7%; Score 28.8; DB 2; Length 184;
 Best Local Similarity 65.8%; Pred. No. 2.8e+03;
 Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 91 GATGAGCGAGATGACCACTCCGCGCCGCGACTCGACGATGAGCGAGATGACCACTCCG 150
 DB 103 CGTGAGGAAGAGACCACTCGCGCGGTGGTGGAGGAAGAGACCACTCCG 162
 QY 151 GCCG 154
 DB 163 GCCG 166

RESULT 20
 BF882476 184 bp mRNA linear EST 17-JAN-2001
 LOCUS BF882476
 DEFINITION CM1-ET0191-051200-626-b02 ET0191 Homo sapiens cDNA, mRNA sequence.
 ACCESSION BF882476
 VERSION BF882476.1 GI:12272602
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS 1 (bases 1 to 184)
 Dias Neto,E., Garcia Correa,R., Verjowski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 MEDLINE 20202663
 PUBMED 10737800
 COMMENT Contact: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the PABSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?l=CM1&t2=CM1-ET0191-051200-626-b02&t3=2000-12-05&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 24
 High quality sequence stop: 180.
 Location/Qualifiers

FEATURES

source

1. 184
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0191"
/note="Organ: Lung tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 18.7%; Score 28.8; DB 2; Length 184;
Best Local Similarity 65.6%; Pred. No. 2.8e+03;
Matches 42; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

1 CGGCGGAGCTGTCATCTCGTCTCATCTGAGTGGCGGCGGAGCTGTCATCTGCT 60
166 CGGCGGAGCTGTCATCTCTTCTCTCTCCACACCCAGCTACCGCCGATGTCCTTCCCT 107

Qy 61 CATC 64
106 CACC 103

Db

RESULT 21
BI777398 194 bp mRNA linear EST 23-JUN-2002
LOCUS EBRO04_S0001_B16_R root, 3 week, salt-stressed, cv Optic, EBRO04
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBRO04_S0001_B16 5', mRNA
sequence.
ACCESSION BI777398
VERSION BI777398.2 GI:21948919
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 194)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Sep 26, 2001 this sequence version replaced gi:15780290.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1. 194
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBRO04_S0001_B16"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBRO04"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome

resources of BBSRC/SBERAD funded cereal IGF (Investigating Gene Function) project."

ORIGIN

Query Match 18.7%; Score 28.8; DB 4; Length 194;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 72; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

2 GCGCGAGCTGTCATCTCGTCTCATCTGAGTGGCGGCGGAGCTGTCATCTGCTC 61
45 GAGAGCGCGGCTTTCTTCTTCTCGCGCGCATAGAGTCTGTGAGCTGGAGCTTGAAC 104
62 ATCTCGAGTGGCGGCGCGCGCACTCGACGATGACGAGATGACAGCTCCGCGCGCA 121
105 ATGAGCGGAGAGTGCAGACCGCGGAGAGTGTGATAGTGTGAGTGTGAGTGTGCGGC 164

Qy 122 CTCGACGATGACGAGATGACAG 145
165 TTCAGGAGAGATGACAGGCGCCG 188

Db

RESULT 22
BI777398/c 194 bp mRNA linear EST 23-JUN-2002
LOCUS EBRO04_S0001_B16_R root, 3 week, salt-stressed, cv Optic, EBRO04
DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBRO04_S0001_B16 5', mRNA
sequence.
ACCESSION BI777398
VERSION BI777398.2 GI:21948919
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
1 (bases 1 to 194)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
On Sep 26, 2001 this sequence version replaced gi:15780290.
Contact: Waugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: est@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
1. 194
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Optic"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="EBRO04_S0001_B16"
/tissue_type="root"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="root, 3 week, salt-stressed, cv Optic, EBRO04"
/note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I;
Non-normalised library, directionally cloned into pSPORT1.
Derived from roots of 3 week old salt stressed barley
plants. Developed as part of the barley transcriptome
resources of BBSRC/SBERAD funded cereal IGF (Investigating
Gene Function) project."

ORIGIN

Query Match 18.7%; Score 28.8; DB 4; Length 194;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 72; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 10 CTGTCATCTGCTCATGCTGAGTCGGCGCCGAGCTGTCATCTGCTCATGCTGA 69
 Db 188 CGGGCCCTGCAGCTCTCTCGTGAAGCCGAGACATCGACCGCACCCTTACCACTCTC 129
 QY 70 GTCCGCGCGCCGCGACTCGACGATGAGCAGATGACCAAGCTCCGCGCCGACTCGACGA 129
 Db 128 GCGGCTTGCACTCTCGGCTTCATGTCAGAGCCTCCAGCTCAGACACTTATGCGCG 69
 QY 130 TGAGCGAGATGACGAGCTCCGCGCC 153
 Db 68 CGAGAAAGAAAACCGCGCCTCC 45

RESULT 23
 CE208692 179 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000372681097 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE208692
 VERSION
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 179)
 Ruchsh,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)

TITLE JOURNAL
 MEDLINE
 PUBMED
 14512627
 CONTACT: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: shotgun.

FEATURES
 source Location/Qualifiers
 1..179
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_1lb="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 18.6%; Score 28.6; DB 9; Length 179;
 Best Local Similarity 57.1%; Pred.No. 3.2e+03;
 Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 55 CTCGCTATGCTCGAGTCGGCGCGCGAGCTCGACATGAGCAGATGACCACTCCG 114
 Db 13 CGCGGAGAGCTCGCTCGCTTGTTGGAGAGGAGTGGAGCGAGCGGAGCCGAGTCTCAG 72
 QY 115 CCGCGCACTCGACGATGAGCAGATGACCAAG 145
 Db 73 CAGCCGCGCGCATGCGAGTGTCCCCAG 103

RESULT 24
 CE208692 179 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000372681097 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE208692
 VERSION
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 1 (bases 1 to 179)
 Ruchsh,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)

TITLE JOURNAL
 MEDLINE
 PUBMED
 14512627
 CONTACT: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirkness@tigr.org
 Class: shotgun.

FEATURES
 source Location/Qualifiers
 1..179
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_1lb="Dog Library"
 /note="Site 1: BstXI; Libraries were prepared from
 peripheral blood"

ORIGIN
 Query Match 18.6%; Score 28.6; DB 9; Length 179;
 Best Local Similarity 57.1%; Pred.No. 3.2e+03;
 Matches 52; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 10 CTGTCATCTGCTCATGCTGAGTCGGCGCGAGCTGTCATCTGCTCATGCTGA 69
 Db 103 CTGGGAGACTCATCTCGCATGCGCGCGCTGCTAGACTCCGGGTCCGCTTCTGCTCA 44
 QY 70 GTCCGCGCGCCGCGACTCGACGATGAGCGAG 100
 Db 43 CTCGCTCCCAAGCGAGCGACGCTGCCCGCG 13

RESULT 25
 CA004311 190 bp mRNA linear EST 23-OCT-2002
 LOCUS H817D13 HS Hordeum vulgare subsp. vulgare cDNA clone H817D13
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION CA004311
 VERSION CA004311.1 GI:24281293
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Poales; Poaceae; Hordeum.
 1 (bases 1 to 190)
 Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
 Graner,A.
 Barley ESTs from germinating seeds
 Unpublished (2002)
 CONTACT: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert Length: 190 Std Error: 0.00
 Plate: 17 row: D column: 13
 Seq primer: M13rev.

QY 97 CGAGATGACCGAGCTCGCGCCGCACTCG 125
Db 96 CTACGTCCTCCAGCTCCAGCCGCGGCTCG 124

RESULT 28
CN423515/C
LOCUS CN423515 147 bp mRNA linear EST 16-MAY-2004
DEFINITION 17000600057518 GRN_PREHP Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN423515
VERSION CN423515.1 GI:47411109
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Branderberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Branderberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8686
Fax: 650 473 7760
Email: rbranderberger@geron.com
Insert Length: 147 Std Error: 0.00.
Location/Qualifiers
1. 147
/organism="Homo sapiens"
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/tissue_type="embryonic stem cells, DMSO-treated H9 cell
line"
/clone_lib="GRN_PREHP"
/note="Oligo dT primed, full-length enriched cDNA library
from DMSO-treated H9 cell line H9 (p22) maintained in
feeder-free conditions"

ORIGIN
Query Match 18.3%; Score 28.2; DB 7; Length 147;
Best Local Similarity 57.3%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCGCGAGCTGTCATCTCGTCATCTCGAGTCGCGCGCGCACTCGA 89
Db 124 CGAGCCGCGCGCTGAGCTGGGAGCGTAGACTTAGTGAGCCGAGGAGAGAAATCC 65
QY 90 CGATGAGCGAGATGACCACTCGCGCGCCG 118
Db 64 CGCCGAAACGCGAGACACCGCCGCGCAGC 36

RESULT 29
LOCUS A1564785 196 bp mRNA linear EST 12-MAY-1999
DEFINITION tn37c01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169792 3',
mRNA sequence.
ACCESSION A1564785
VERSION A1564785.1 GI:4523242
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological

JOURNAL
COMMENT Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 277 Std Error: 0.00
Seq primer: -400P from Gibco
POLYA=No.
Location/Qualifiers
1. 196
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/db_xref="taxon:9606"
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/note="Organ: Brain; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site: 1; Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - Oligo(dT) primer [5'
TGTTCACCAATCTGAGTGGAGCGCGCATGATGTTTCTTTTCTTTTCTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
Library is normalized, and was constructed by Bento
Soares and M.Fatima Bonaldo."

ORIGIN
Query Match 18.3%; Score 28.2; DB 1; Length 196;
Best Local Similarity 57.3%; Pred. No. 4e+03; Indels 0; Gaps 0;
Matches 51; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 30 CGAGTCGGCGCGCGAGCTGTCATCTCGTCATCTCGAGTCGCGCGCGCACTCGA 89
Db 104 CGAGCCGCGCGCTGAGCTGGGAGCGTAGACTTAGTGAGCCGAGGAGAGAAATCC 163
QY 90 CGATGAGCGAGATGACCACTCGCGCGCCG 118
Db 164 CGCCGAAACGCGAGACACCGCCGCGCAGC 192

RESULT 30
LOCUS A1564785/C 196 bp mRNA linear EST 12-MAY-1999
DEFINITION tn37c01.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone IMAGE:2169792 3',
mRNA sequence.
ACCESSION A1564785
VERSION A1564785.1 GI:4523242
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BRGAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

KEYWORDS	ST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 130)
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bata, G. S., Simpson, D. H., Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
TITLE	Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE	20202663
PUBMED	10737800
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This sequence was derived from the PAPPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?l1=RC&t2=RC2-CT0652-211200-011-201&t3=2000-12-21&t4=1) Seq primer: puc 18 forward High quality sequence start: 23 High quality sequence stop: 130. Location/Qualifiers 1. 130 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_idb="CT0652" /notes="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
ORIGIN	
Query Match	18.2%; Score 28; DB 2; Length 130;
Best Local Similarity	63.2%; Pred. No. 4.5e+03;
Matches	43; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
Oy	3 GCCGAGACTGTCATCTCGCTCATCGTCAGTCGGCGCGGAGAGCTGTCATCTCGCTCA 62
Db	91 GCCCGAGAGTGTCATCTCTCTCACACCCAGCATATCACGCCCAAGTGTCTTTCCTCA 32
Oy	63 TCGTCGAG 70
Db	31 CCACCCAG 24
RESULT 37	
LOCUS	CB251950 110 bp mRNA linear EST 19-FEB-2003
DEFINITION	3529_1_19_1.H10.Y.1 3529 - 2 mm ear tissue from Schmidt and Hake
ACCESSION	CB251950
VERSION	CB251950.1 GI:28422637
KEYWORDS	EST.
SOURCE	Zea mays
ORGANISM	Zea mays
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

Db 66 CTGTCATGTCGGTCTTCACGTAGCCCGGTCGCGCATGTTGACGCGCAGCTCGGGTGC 125

Qy 107 AGCTCCGCGCCGCGCATCTGACGATGAG 133

Db 126 CGCTCGCCAGACCTCGAGTAGAG 152

RESULT 40
AI834106/c 161 bp mRNA linear EST 02-FEB-2000

LOCUS AI834106

DEFINITION 606065A12.x1 606 - Ear tissue cDNA library from Schmidt lab Zea

ACCESSION mays cDNA, mRNA sequence.

VERSION AI834106

KEYWORDS AI834106.1 GI:5456416

SOURCE EST.

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 161)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 606065 row: A column: 12.

FEATURES
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Location/Qualifiers
1..161
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/db_xref="taxon:4577"
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/lab_host="XLOLR (Stratagene)"
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/note="Organ: immature ear; Vector: pBK-CMV; Site_1: ECKR1; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"

ORIGIN

Query Match 18.1%; Score 27.8; DB 1; Length 161;
Best Local Similarity 57.5%; Pred. No. 5e+03;
Matches 50; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 22 CTGATCTCGAGTCGCGCGCGCATCTGCTCATCTCGAGTCGCGCGCGC 81

Db 152 CTCTACTCGAGGTCCTCGCGAGCGCGCACCCGAGCTGCGCTCACTCGCGCACCC 93

Qy 82 CGACTCGACGATGACGAGATGACAG 108

Db 92 GGGCTACGTGAGACCGACATGACAG 66

RESULT 41
BF728943 163 bp mRNA linear EST 09-JAN-2001

LOCUS BF728943

DEFINITION 1000069F04.x2 1000 - Unigene 1 from Maize Genome Project Zea mays

ACCESSION cDNA, mRNA sequence.

VERSION BF728943

KEYWORDS BF728943.1 GI:12046804

SOURCE EST.

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

REFERENCE 1 (bases 1 to 163)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1000069 row: F column: 04.

FEATURES
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Location/Qualifiers
1..163
/organism="Zea mays"
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/db_xref="dbEST:945002F06.X3"
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/note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the Unigene set. All singlets were also selected."

ORIGIN

Query Match 18.1%; Score 27.8; DB 2; Length 163;
Best Local Similarity 62.0%; Pred. No. 5e+03;
Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 49 GGTCTCTCGCTCATCTGCGCGCGCGCATCTGACGATGACGATGACAG 108

Db 65 GCTTACTCTCGCGCGCGCATGACCGCGGCTTACTGCTGAGCGATGACAGG 124

Qy 109 CTCGCGCGCGC 119

Db 125 CGGCATCCGC 135

RESULT 42
BF728943/c 163 bp mRNA linear EST 09-JAN-2001

LOCUS BF728943/c

DEFINITION 1000069F04.x2 1000 - Unigene 1 from Maize Genome Project Zea mays

ACCESSION cDNA, mRNA sequence.

VERSION BF728943

KEYWORDS BF728943.1 GI:12046804

SOURCE EST.

ORGANISM Zea mays

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 163)

AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University

JOURNAL Unpublished (1999)

COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 1000069 row: F column: 04.

FEATURES
source
Location/Qualifiers
1..163

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/organism="Zea mays"
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/db_xref="dbEST:1945002F06.X3"
/db_xref="taxon:4577"
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/note="This library represents the unique ESTs found in the first round of EST sequencing at Stanford University for the maize genome project. Sequences are present from 11 libraries 486, 487, 496, 603, 605, 606, 614, 618, 660, 683, 687, 707, and 945. Contigs were assembled using TIGR's CAP program and a representative EST from each contig was selected for the unigene set. All singlets were also selected."

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	ORIGIN
Query Match	18.1%; Score 27.8; DB 2; Length 163;
Best Local Similarity	62.0%; Pred. NO. 5e+03;
Matches 44; Conservative	0; Mismatches 27; Indels 0; Gaps 0.

OY
36 GGGCGGCGAGACTGATCTCTCGGTATTCGTACGATCGGCGGCCGCAGATTCCAGCATTA 95

Dδ
135 GCCCGAATGCGCCCCCTTAACTGCTCAGCGCTGAAGTACCCTCGTGCGGCTTTAACGCCCG 76

OY
96 GCAGAGATGACC 106

Dδ
75 CGAGAGTAGC 65

RESULT 43									
AJ469411									
LOCUS	AJ469411	180 bp	mRNA	linear	EST 24-MAY-2002				
DEFINITION	AJ469411 S00008 Hordeum vulgare cDNA clone S000080004.F1.F11, mRNA								

ACCESSION	AJ469411	
VERSION	AJ469411.1	GI:21185367
KEYWORDS	EST.	
SOURCE	Hordeum vulgare	
ORGANISM	Hordeum vulgare	Stachyosebif, Embryonbif, Tracheonbif

REFERENCE	1 (bases 1 to 180)
AUTHORS	Saren,A.-M., Tanskanen,J., Paulin,L. and Schulman,A.H
TITLE	Barley EST's
JOURNAL	Unpublished (2002)
COMMENT	Contact: Schulman AH

University of Helsinki
P.O. Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014
Finland.

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FEATURES
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ORIGIN

Query Match	18.1%	Score 27.8	DB 1	Length 180
Best Local Similarity	57.5%	Pred. No. 5e+03		
Matches 50	Conservative 0	Mismatches 37	Indels 0	Gaps 0

Oy 46 GCTTGATCTCGTCA TGCAGTCGGCCGCCGACTCAGCATGAACGAGATGAC 105
 ||| | | | | | | | | | | |
Db 24 GCCGGCGA CCCCCCG CGCGAGA GAAAGAACAGCGCATTCACATCAA GGCGCTTGGC 83

QY		106 CAGCTCCGGCGGCCGACTGCATGA	132
Db		84 CATCTCCGGCGGCCGCTTAACCTGA	110

RESULT 44
AJ469411/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AJ469411 180 bp mRNA EST 24-MAY-2002
AJ469411 S00008 Hordeum vulgare cDNA clone S0000800047F11FL, mRNA
sequence.
AJ469411
AJ469411.1 GI:21185367
EST.
Hordeum vulgare
Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Hordeum.
1 (bases 1 to 180)
Saren, A.-M., Tansekänen, J., Paulin, L. and Schulman, A.H.
Barley EST's
Unpublished (2002)
Contract: Schulman AH
Institute of Biotechnology
University of Helsinki
P.O. Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
Finland.

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FEATURES
  source
    Location/Qualifiers
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        /mol_type="mRNA"
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        /clone="S0000800047F11F1"
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Query Match	18.1%	Score 27.8	DB 1	Length 180
Best Local Similarity	57.5%	Pred. No. 5e+03	Mismatches 37	Indels 0
Matches	50	Conservative	0	Gaps 0
QY	23	TCATGTTGAGAGCGGCGCGAGCGTGTCACTTCGTCAATCGTGAATCGAGCGCGCC	82	
DB	110	TCAGAGTGAAGGCGCGCGCGAGATGCGCACGCGCCCTTGATGATGATGAGCGGCTCGCTCC	51	
QY	83	GACTCGACGATGACGAGATGACACAGC	109	
DB	50	TCCTCGCGCGCGGCGCGCTCGGCGCGC	24	

RESULT 45	CC157563	CC157563	184 bp	DNA	linear	GSS 29-APR-2003
LOCUS						
DEFINITION	CC157563	ig24e03.b1 WGS-ZmapAF (DH5a methyl)		filtered		Zea mays genomic clone
ACCESSION	CC157563	ig24e03, genomic survey sequence.				
VERSION	CC157563.1	GI:30182143				
KEYWORDS	GSS.					
SOURCE	Zea mays					
ORGANISM	Zea mays					

ORGANISM *Zea mays*; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 : Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; *Zea*.
 1 (bases 1 to 184)
REFERENCE Rabinowicz, P.D., O'Shaughnessy, A.L., Ballja, V., Dedhia, N.,
AUTHORS Katzenburger, F., King, L.R., Miller, B., Muller, S., Nascimben, L.,
 Zuber, F., McCombie, W.R. and Martienssen, R.A.
TITLE Genomic shotgun sequences from *Zea mays* (methyl-filtered)
JOURNAL Unpublished (2002)
COMMENT Contact: W. Richard McCombie

COMMENT

Contact: W. Richard McCombie
Lita Anenberger Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org

Plate: ig24 row: e column: 03
 Seq primer: -21M3UnivFwd
 Class: Shotgun
 High quality sequence stop: 184.
 Location/Qualifiers

FEATURES
 source

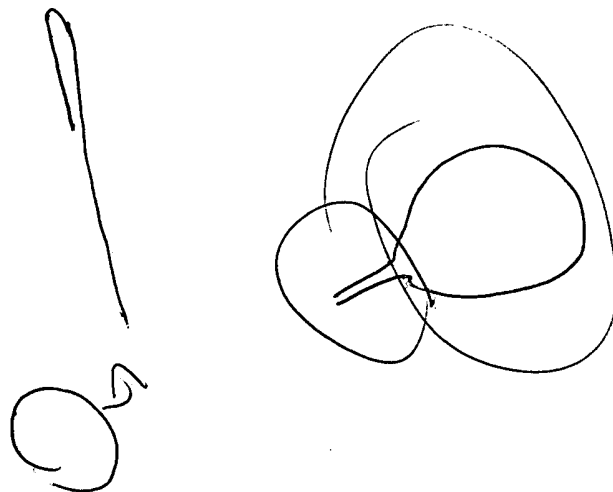
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 /clone_id="MGS-ZmaveF (DH5a methyl filtered)"
 /note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
 The vector was digested with Xba I and one nucleotide was
 added by fill in in the recessive 3' end. The genomic DNA
 was nebulized, end repaired, adaptor ligated and size
 fractionated using sephadex. The resulting fragments were
 between 0.8 and 3 kb and were cloned into the vector (.x/y
 reads in M13mp19. b/g reads in pUC19). The same ligation
 was transformed into DH5a."

ORIGIN

Query Match 18.1%; Score 27.8; DB 8; Length 184;
 Best Local Similarity 62.0%; Pred. No. 5e+03; 27; Indels 0; Gaps 0;
 Matches 44; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

OY	67	CGAGTCGGCGCGCGCGAGCTGACGATGAGCGAGTACCACTCGGCGCGCGAGTGA	126
Db	112	CGACGCGCGCGTGGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCG	171
OY	127	CGATGAGCGAG	137
Db	172	CGACGAGCGCG	182

Search completed: April 9, 2005, 02:31:57
 Job time : 3011 secs



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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 9, 2005, 01:03:52 ; Search time 494 Seconds
(without alignments)
1889.151 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggccgcagcgcgcacatc.....gagatgacacgcgcgcgcg 154

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 5800676

Minimum DB seq length: 0

Maximum DB seq length: 200

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications NA:*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

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11: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

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13: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*

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22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	10	US-09-887-194A-13
2	154	100.0	154	10	US-09-887-194A-13
3	154	100.0	154	10	US-09-934-900-25
4	154	100.0	154	10	US-09-934-900-25
5	154	100.0	154	18	US-10-734-947-7
6	154	100.0	154	18	US-10-734-947-7
7	154	100.0	154	19	US-10-981-293-25
8	154	100.0	154	19	US-10-981-293-25
9	80	51.9	80	10	US-09-887-194A-12
10	80	51.9	80	10	US-09-887-194A-12
11	80	51.9	80	10	US-09-934-900-24

12	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appl
13	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appl
14	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appl
15	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl
16	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl
17	28.4	18.4	191	18	US-10-425-115-158821	Sequence 158821, Appl
18	28.4	18.4	191	18	US-10-425-115-158821	Sequence 158821, Appl
19	27.4	17.8	175	18	US-10-437-963-9894	Sequence 9894, Appl
20	27.4	17.8	175	18	US-10-437-963-9894	Sequence 9894, Appl
21	26	16.9	195	18	US-10-437-963-31230	Sequence 31230, Appl
22	26	16.9	195	18	US-10-437-963-31230	Sequence 31230, Appl
23	25	16.2	123	10	US-09-876-235-34	Sequence 34, Appl
24	25	16.2	123	10	US-09-876-235-34	Sequence 34, Appl
25	25	16.2	123	18	US-10-764-799-34	Sequence 34, Appl
26	25	16.2	123	18	US-10-764-799-34	Sequence 34, Appl
27	24.8	16.1	108	16	US-10-029-386-21853	Sequence 21853, Appl
28	24.8	16.1	108	16	US-10-029-386-21853	Sequence 21853, Appl
29	24.6	16.0	167	18	US-10-767-701-21754	Sequence 21754, Appl
30	24.6	16.0	167	18	US-10-767-701-21754	Sequence 21754, Appl
31	24.4	15.8	164	9	US-09-923-876-4668	Sequence 4668, Appl
32	24.4	15.8	164	9	US-09-923-876-4668	Sequence 4668, Appl
33	24.4	15.8	164	10	US-09-923-876-4668	Sequence 4668, Appl
34	24.4	15.8	164	10	US-09-923-876-4668	Sequence 4668, Appl
35	24.4	15.8	183	18	US-10-425-115-62701	Sequence 62701, Appl
36	24.4	15.8	183	18	US-10-425-115-62701	Sequence 62701, Appl
37	24.4	15.8	185	9	US-09-864-761-25686	Sequence 25686, Appl
38	24.4	15.8	185	9	US-09-864-761-25686	Sequence 25686, Appl
39	24.2	15.7	175	18	US-10-753-646-15	Sequence 15, Appl
40	24.2	15.7	175	18	US-10-753-646-15	Sequence 15, Appl
41	24.2	15.7	183	18	US-10-425-115-140476	Sequence 140476, Appl
42	24.2	15.7	183	18	US-10-425-115-140476	Sequence 140476, Appl
43	23.6	15.3	192	15	US-10-156-761-3130	Sequence 3130, Appl
44	23.6	15.3	192	15	US-10-156-761-3130	Sequence 3130, Appl
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48	23.4	15.2	159	18	US-10-437-963-58822	Sequence 58822, Appl
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53	23.2	15.1	166	18	US-10-767-701-18290	Sequence 18290, Appl
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55	23.2	15.1	192	9	US-09-920-300A-496	Sequence 496, Appl
56	23.2	15.1	192	9	US-09-920-300A-496	Sequence 496, Appl
57	23.2	15.1	192	13	US-10-033-528-496	Sequence 496, Appl
58	23.2	15.1	192	13	US-10-033-528-496	Sequence 496, Appl
59	23.2	15.1	192	16	US-10-099-926-496	Sequence 496, Appl
60	23.2	15.1	192	16	US-10-099-926-496	Sequence 496, Appl
61	23	14.9	74	17	US-10-434-156-28	Sequence 28, Appl
62	23	14.9	74	17	US-10-434-156-28	Sequence 28, Appl
63	23	14.9	176	10	US-09-862-540-7	Sequence 7, Appl
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65	23	14.9	192	18	US-10-425-115-81742	Sequence 81742, Appl
66	23	14.9	192	18	US-10-425-115-81742	Sequence 81742, Appl
67	23	14.9	192	18	US-10-425-115-95527	Sequence 95527, Appl
68	23	14.9	192	18	US-10-425-115-95527	Sequence 95527, Appl
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76	22.8	14.8	199	18	US-10-425-115-97978	Sequence 97978, Appl
77	22.6	14.7	180	15	US-10-156-761-4433	Sequence 4433, Appl
78	22.6	14.7	180	15	US-10-156-761-4433	Sequence 4433, Appl
79	22.6	14.7	183	17	US-10-140-410-1	Sequence 1, Appl
80	22.6	14.7	183	17	US-10-140-410-1	Sequence 1, Appl
81	22.6	14.7	200	11	US-09-987-899-107	Sequence 107, Appl
82	22.6	14.7	200	11	US-09-987-899-107	Sequence 107, Appl
83	22.4	14.5	110	19	US-10-950-009-970	Sequence 970, Appl
84	22.4	14.5	110	19	US-10-950-009-970	Sequence 970, Appl

85 22.4 14.5 114 18 US-10-741-601-2931 Sequence 2931, Ap
 C 86 22.4 14.5 114 18 US-10-741-601-2931 Sequence 2931, Ap
 87 22.4 14.5 114 18 US-10-741-601-3022 Sequence 3022, Ap
 C 88 22.4 14.5 114 18 US-10-741-601-3022 Sequence 3022, Ap
 89 22.4 14.5 114 18 US-10-741-601-3115 Sequence 3115, Ap
 C 90 22.4 14.5 114 18 US-10-741-601-3115 Sequence 3115, Ap
 91 22.4 14.5 114 19 US-10-741-600-11671 Sequence 11671, A
 C 92 22.4 14.5 114 19 US-10-741-600-11671 Sequence 11671, A
 93 22.4 14.5 114 19 US-10-741-600-11762 Sequence 11762, A
 C 94 22.4 14.5 114 19 US-10-741-600-11762 Sequence 11762, A
 95 22.4 14.5 114 19 US-10-741-600-11855 Sequence 11855, A
 C 96 22.4 14.5 114 19 US-10-741-600-11855 Sequence 11855, A
 97 22.4 14.5 151 18 US-10-425-115-3104 Sequence 3104, Ap
 C 98 22.4 14.5 151 18 US-10-425-115-3104 Sequence 3104, Ap
 99 22.4 14.5 161 17 US-10-424-599-56083 Sequence 56083, A
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ALIGNMENTS

RESULT 1

US-09-887-194A-13
 ; Sequence 13, Application US/09887194A
 ; Publication No. US20030036197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glasman, Kimberly F.
 ; APPLICANT: Gordon-Kamm, William J.
 ; APPLICANT: Kinney, Anthony
 ; APPLICANT: Lowe, Keith S.
 ; APPLICANT: Nichols, Scott E.
 ; APPLICANT: Stecca, Kevin L.
 ; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
 ; FILE REFERENCE: B1449 US NA
 ; CURRENT APPLICATION NUMBER: US/09/887,194A
 ; CURRENT FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 13
 ; LENGTH: 154
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
 ; OTHER INFORMATION: region of pKS133
 US-09-887-194A-13

Query Match 100.0%; Score 154; DB 10; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2,2e-37;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 60
 DB 1 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 60
 QY 61 CATGTCAGTGGGGCGGCGGCGGCGGAGCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 120
 DB 61 CATGTCAGTGGGGCGGCGGCGGCGGAGCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 120
 QY 121 ACTGACGATGAGCGAGATGACCACTCCGGCCG 154
 DB 121 ACTGACGATGAGCGAGATGACCACTCCGGCCG 154

RESULT 2

US-09-887-194A-13/c
 ; Sequence 13, Application US/09887194A
 ; Publication No. US20030036197A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glasman, Kimberly F.
 ; APPLICANT: Gordon-Kamm, William J.
 ; APPLICANT: Kinney, Anthony
 ; APPLICANT: Lowe, Keith S.

; APPLICANT: Nichols, Scott E.
 ; APPLICANT: Stecca, Kevin L.
 ; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
 ; FILE REFERENCE: B1449 US NA
 ; CURRENT APPLICATION NUMBER: US/09/887,194A
 ; CURRENT FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 13
 ; LENGTH: 154
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
 ; OTHER INFORMATION: region of pKS133
 US-09-887-194A-13

Query Match 100.0%; Score 154; DB 10; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2,2e-37;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 60
 DB 154 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 95
 QY 61 CATGTCAGTGGGGCGGCGGCGGCGGAGCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 120
 DB 94 CATGTCAGTGGGGCGGCGGCGGCGGAGCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 35
 QY 121 ACTGACGATGAGCGAGATGACCACTCCGGCCG 154
 DB 34 ACTGACGATGAGCGAGATGACCACTCCGGCCG 1

RESULT 3

US-09-934-900-25
 ; Sequence 25, Application US/09934900
 ; Publication No. US20030054521A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Booth, Russ
 ; APPLICANT: Canoon, Rebecca E
 ; APPLICANT: Hitz, William D
 ; APPLICANT: Kinney, Anthony
 ; APPLICANT: Yadav, Naren
 ; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
 ; FILE REFERENCE: B1476 US NA
 ; CURRENT APPLICATION NUMBER: US/09/934,900
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/226996
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 25
 ; LENGTH: 154
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
 ; OTHER INFORMATION: region of pKS133
 US-09-934-900-25

Query Match 100.0%; Score 154; DB 10; Length 154;
 Best Local Similarity 100.0%; Pred. No. 2,2e-37;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 60
 DB 1 CGGCGGAGCTGTCATCTCGCTCATCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 60
 QY 61 CATGTCAGTGGGGCGGCGGCGGCGGAGCTGTCAGTGGGGCGGCGGAGCTGTCATCTCGCT 120
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Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154

RESULT 4

US-09-934-900-25/c
; Sequence 25, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadau, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-934-900-25

Query Match 100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 60
Db 154 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 95
Qy 61 CATGTCGAGTCGCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 120
Db 94 CATGTCGAGTCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 35
Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 34 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 1

RESULT 5

US-10-734-947-7
; Sequence 7, Application US/10734947
; Publication No. US20040128714A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOPHYLONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOPHYLONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
; FILE REFERENCE: BB1535 US NA
; CURRENT APPLICATION NUMBER: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two

; OTHER INFORMATION: 36-nucleotide repeats and having an EagI site at each end.
US-10-734-947-7

Query Match 100.0%; Score 154; DB 18; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 60
Db 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 60
Qy 61 CATGTCGAGTCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 120
Db 61 CATGTCGAGTCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 120
Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154

RESULT 6

US-10-734-947-7/c
; Sequence 7, Application US/10734947
; Publication No. US20040128714A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOPHYLONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOPHYLONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
; FILE REFERENCE: BB1535 US NA
; CURRENT APPLICATION NUMBER: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two
US-10-734-947-7

Query Match 100.0%; Score 154; DB 18; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 60
Db 154 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGCGCGGAGCTGCTCATCTGCT 95
Qy 61 CATGTCGAGTCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 120
Db 94 CATGTCGAGTCGCGCGCGCGCGCGAGTGAAGGATGACCAAGCTCCGGCGCG 35
Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 34 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 1

RESULT 7

US-10-961-293-25
; Sequence 25, Application US/10961293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadau, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-

TITLE OF INVENTION: ACP Desaturase
FILE REFERENCE: BBI476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-10-981-293-25

Query Match
Best Local Similarity 100.0%; Score 154; DB 19; Length 154;
Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTGCT 60
Qy 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 120
Db 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 120

Qy 121 ACTGACGATGAGGAGATGACGAGTCGCGCGCG 154
Db 121 ACTGACGATGAGGAGATGACGAGTCGCGCG 154

RESULT 8
US-10-981-293-25/c
Sequence 25, Application US/10981293
Publication No. US20050066390A1
GENERAL INFORMATION:
APPLICANT: Booch, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hiltz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadau, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BBI476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 25
LENGTH: 154
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-10-981-293-25

Query Match
Best Local Similarity 100.0%; Score 154; DB 19; Length 154;
Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 154 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTGCT 95

Qy 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 120
Db 94 CATGTCGAGTCGGCGCGGCGGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 35
Qy 121 ACTGACGATGAGGAGATGACGAGTCGCGCGCG 154
Db 34 ACTGACGATGAGGAGATGACGAGTCGCGCGCG 1

RESULT 9
US-09-887-194A-12
Sequence 12, Application US/09887194A
Publication No. US20030036197A1
GENERAL INFORMATION:
APPLICANT: Glaesman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
FILE REFERENCE: BBI449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-12

Query Match
Best Local Similarity 100.0%; Score 80; DB 10; Length 80;
Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGTCGAGTCGAGTCGAGTC 97
Db 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGTCGAGTCGAGTCGAGTC 60
Qy 98 GAGATGACGAGTCGCGCGCG 117
Db 61 GAGATGACGAGTCGCGCGCG 80

RESULT 10
US-09-887-194A-12/c
Sequence 12, Application US/09887194A
Publication No. US20030036197A1
GENERAL INFORMATION:
APPLICANT: Glaesman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nichols, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
FILE REFERENCE: BBI449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 80
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-12

US-09-887-194a-12

Query Match 51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21

Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 20 GAGATGACCAAGCTCCGGCCG 1

RESULT 11

US-09-934-900-24
Sequence 24, Application US/09934900
Publication No. US20030054521A1

GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren

TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA

CURRENT APPLICATION NUMBER: US/09/934,900

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/226996

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

SEQ ID NO 24

LENGTH: 80

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

OTHER INFORMATION: region of pKS106 and pKS124

US-09-934-900-24

Query Match 51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 60

Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 61 GAGATGACCAAGCTCCGGCCG 80

RESULT 12

US-09-934-900-24/c
Sequence 24, Application US/09934900
Publication No. US20030054521A1

GENERAL INFORMATION:

APPLICANT: Booth, Russ

APPLICANT: Cahoon, Rebecca E

APPLICANT: Hitz, William D

APPLICANT: Kinney, Anthony

APPLICANT: Yadav, Naren

TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA

CURRENT APPLICATION NUMBER: US/09/934,900

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/226996

PRIOR FILING DATE: 2000-08-22

NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97

SEQ ID NO 24

LENGTH: 80

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

OTHER INFORMATION: region of pKS106 and pKS124

US-09-934-900-24

Query Match 51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21

Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 20 GAGATGACCAAGCTCCGGCCG 1

RESULT 13

US-10-981-293-24
Sequence 24, Application US/10981293
Publication No. US20050066390A1

GENERAL INFORMATION:

APPLICANT: Booth, Russ

APPLICANT: Cahoon, Rebecca E

APPLICANT: Hitz, William D

APPLICANT: Kinney, Anthony

APPLICANT: Yadav, Naren

TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA

CURRENT APPLICATION NUMBER: US/10/981,293

PRIOR FILING DATE: 2004-11-04

PRIOR APPLICATION NUMBER: US/09/934,900

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/226996

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

SEQ ID NO 24

LENGTH: 80

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

OTHER INFORMATION: region of pKS106 and pKS124

US-10-981-293-24

Query Match 51.9%; Score 80; DB 19; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCCGCACTCGACGATGAGC 60

Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 61 GAGATGACCAAGCTCCGGCCG 80

RESULT 14

US-10-981-293-24/c
Sequence 24, Application US/10981293
Publication No. US20050066390A1

GENERAL INFORMATION:

APPLICANT: Booth, Russ

Query Match	51.9%;	Score 80;	DB 10;	Length 92;
Best Local Similarity	100.0%;	Pred. No. 6.2e-15;		
Matches	80;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	38	CGGCGGAGCTGCGTCATCTGCGTATGTCAGTCGCGCGCGCGCGACTGCAGCATGAGC	97	
Db	7	CGGCGGAGCTGTCATCTGCTCTATCTCGATCGAGTCGGCGCGCGCGACTGCAGCATGAGC	66	
QY	98	GAGATGACCAAGCTTCGSCCG	117	
Db	67	GAGATGACCAAGCTTCGSCCG	86	

Query Match	18.4%	Score 28.4	DB 18	Length 191
Best Local Similarity	52.5%	Pred. No. 27		
Matches	62	Conservative	0	Mismatches 56
				Indels 0
				Gaps 0
QY	21	GCTCATGTGAGTCCGCGCGCCGAGCTGTGTCATCTTCATCATGTCGAGTCGCGCGCGC	80	
Db	17	GCTCCGCTTGACCGGGGGGACATCGGGCGGCATTCGAGCCTACGAGCTGTTCATGAACG	76	
QY	81	CCGACTGACGATGAGGGAATGACCAAGCTTCGCGCCGCCGACTGAGCATTAAGCAGA	138	

[illegible]

```

; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3558C.1
US-10-437-963-31230

```

Query Match 16.9%; Score 26; DB 18; Length 195;
Best Local Similarity 54.1%; Pred. No. 1.4e+02;
Matches 53; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 51 TCATCTCGCTCATGCTGAGTCGCGCGCCGCACTCGACGATGAGCAGATGACCACT 110
DB 41 TCGCCGCTGCTCCCTCGCTGCTGAGCGGAGCCGACACGCGCGCGCCGCTCT 100

QY 111 CCGGCGCGCACTCGACGATGAGCAGATGACCACTC 148
DB 101 CCGACGCGCGCCCGCTTTAAAGACATGAGTATGCG 138

RESULT 22
US-10-437-963-31230/c
; Sequence 31230, Application US/10437963
; Publication No. US2004012343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIORITY FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 31230
; LENGTH: 195
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MKT4530_35558C.1
US-10-437-963-31230

Query Match 16.9%; Score 26; DB 18; Length 195;
Best Local Similarity 54.1%; Pred. No. 1.4e+02;
Matches 53; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

QY 7 GAGCTGCTCATGCTGCTCATGCTGAGTCGCGCGCGGAGCTGCTCATCTGCTCATGCT 66
DB 138 GCGATACCTCATGCTCTTTAAAGCGGCGCGCGCTCGAGACGCGCGCGCTGCGCGCGC 79

QY 67 CGAGTCGCGCGCGCGCGCACTGACGATGAGCGGAGATGA 104
DB 78 GTGGTCGCTGCTCCGCTGACGCGAGGAGGAGCGCGCG 41

RESULT 23
US-09-876-235-34
; Sequence 34, Application US/09876235
; Publication No. US2003002236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE OF INVENTION: FUSIONS
; CURRENT APPLICATION NUMBER: US/09/876,235
; PRIORITY FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005

PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-09-876-235-34

Query Match 16.2%; Score 25; DB 10; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

QY 18 CTCGCTCATGCTGAGTCGCGCGCGGAGCTGCTCATCTGCTCATGCTGAGTCGCGCG 77
DB 12 CTGTGCTCATGCTGAGTCGCGCGCGGAGCTGCTCATCTGCTCATGCTGAGTCGCGCG 71

QY 78 CCGCGCACTGACGATGAGCAGATGACCACTCCGCGCGCGCACTC 124
DB 72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 118

RESULT 24
US-09-876-235-34/c
; Sequence 34, Application US/09876235
; Publication No. US2003002236A1
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihc
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE OF INVENTION: FUSIONS
; CURRENT APPLICATION NUMBER: US/09/876,235
; PRIORITY FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 123
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-09-876-235-34

Query Match 16.2%; Score 25; DB 10; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

QY 31 GAGTCGCGCGCGCGGAGCTGCTCATCTGCTCATGCTGAGTCGCGCGCGGAGCTCGAC 90
DB 118 GACCAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 59

QY 91 GATGAGCAGATGACCACTCCGCGCGCGGAGCTCGACGATGAGCGAG 137
DB 58 SNNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 12

RESULT 25
US-10-764-799-34
; Sequence 34, Application US/10764799
; Publication No. US20040253612A1
; GENERAL INFORMATION:

APPLICANT: Szoestak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihé
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350005
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 123
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-10-764-799-34

Query Match 16.2%; Score 25; DB 18; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

Qy 18 CTCGCTATCGTCAGTCGCGCGGAGTCGTCATCTCGTCATCGTCGCGG 77
Db 12 CTGTGATCGTCCNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 71
Qy 78 CCGCGGACTCGACGATGAGCGAGATGACCACTCGCGCGCGGCACTC 124
Db 72 NSNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCTCTCGCCCTGCTC 118

RESULT 26
US-10-764-799-34/c
Sequence 34, Application US/10764799
Publication No. US20040253612a1
GENERAL INFORMATION:
APPLICANT: Szoestak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihé
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350005
CURRENT APPLICATION NUMBER: US/10/764,799
CURRENT FILING DATE: 2004-01-26
PRIOR APPLICATION NUMBER: US/09/247,190
PRIOR FILING DATE: 1999-02-09
PRIOR APPLICATION NUMBER: 60/035,963
PRIOR FILING DATE: 1997-01-21
PRIOR APPLICATION NUMBER: 60/064,491
PRIOR FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: 09/007,005
PRIOR FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 123
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: n = a, g, t, or c. s = c or g.
US-10-764-799-34

Query Match 16.2%; Score 25; DB 18; Length 123;
Best Local Similarity 15.0%; Pred. No. 2.9e+02;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

Qy 31 GAGTCGCGCGCGGAGCTGTCATCTCGTCATCGTCGAGTCGCGCGGCACTCGAC 90
Db 118 GAGCAAGCGCGGAGGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 59
Qy 91 GATGAGCGAGATGACCACTCGCGCGCGGCACTCGACGATGAGGAG 137
Db 58 SNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGATGACACAG 12

RESULT 27
US-10-029-386-21853
Sequence 21853, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
FILE REFERENCE: AROMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21853
LENGTH: 108
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR19.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.5
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
OTHER INFORMATION: NT HIT: APL6267.1, EVALUE 2.00e-08
OTHER INFORMATION: SWISSPROT HIT: 005090, EVALUE 3.00e-03
OTHER INFORMATION: EST_HUMAN HIT: BG122566.1, EVALUE 4.00e-54
US-10-029-386-21853

Query Match 16.1%; Score 24.8; DB 16; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.4e+02;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 106 CAGCTCCGCGCGGAGCTCGACGATGAGCGAGATGACGAGCTTC 149
Db 5 CTGCTCTCGCGCGGCTCGCTCGAGCGCGGAGACCACTTC 48

RESULT 28
US-10-029-386-21853/c
Sequence 21853, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GI
FILE REFERENCE: AROMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 21853
LENGTH: 108
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO CHR19.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.2

! FEATURE:
! OTHER INFORMATION: Clone ID: 13318234
! US-10-767-701-21754

; PRIOR APPLICATION NUMBER: 807
 ; PRIOR FILING DATE: 1998-05-05

Db 79 ATCTACAGCGGCGGCTGAGG 100

RESULT 36
US-10-425-115-62701/c
; Sequence 62701, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovallie, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 62701
; LENGTH: 183
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: M74577_157185C.1
US-10-425-115-62701

Query Match 15.8%; Score 24.4; DB 18; Length 183;
Best Local Similarity 56.1%; Pred. No. 4.4e+02;
Matches 46; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 27 CGTCGAGTCGCGCGGCGGAGCTGCTCATCTGCTCATCTGCTCATCTGCGCGCGCGGACT 86
Db 100 CCTGAGCGCCCGCGGCTGTAGATGCGGACGAGCACCCTTCCGCGCCCTTCCGCGCT 41

Qy 87 CGAGCATGAGCGAGATGACGAG 108
Db 40 CGCCGTCGAGCGAGGTATCCG 19

RESULT 37
US-09-864-761-25686
; Sequence 25686, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 25686
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000350.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
; OTHER INFORMATION: NT HIT: AF240786.1, EVALUATE 1.00e-100
; OTHER INFORMATION: SWISSPROT HIT: P30046, EVALUATE 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV655183.1, EVALUATE 1.00e-100
US-09-864-761-25686

Query Match 15.8%; Score 24.4; DB 9; Length 185;
Best Local Similarity 53.5%; Pred. No. 4.4e+02;
Matches 76; Conservative 0; Mismatches 61; Indels 5; Gaps 1;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCGCGGCGGCGGAGCTGCTATC 55
Db 19 CGGCGGAGCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTATC 78

Qy 56 TCGCTATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTATC 115
Db 79 TCGCTATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTCATCTGCTATC 138

Qy 116 CGCGAGTCTGAGATGAGGAG 137
Db 139 GAGTTTCTCACCAGAGCTAG 160

RESULT 38
US-09-864-761-25686/c
; Sequence 25686, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30

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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annamex Sequence Listing Engine vers. 1.1
; SEQ ID NO 25686
; LENGTH: 185
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AP000350.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.6
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.6
; OTHER INFORMATION: NT HIT: AF240786.1, EVALUATE 1.00e-100
; OTHER INFORMATION: SWISSPROT HIT: P30046, EVALUATE 8.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: AV655183.1, EVALUATE 1.00e-100
; US-09-864-761-25686

Query Match 15.8%; Score 24.4; DB 9; Length 185;
Best Local Similarity 53.5%; Pred. No. 4.4e+02;
Matches 76; Conservative 0; Mismatches 61; Indels 5; Gaps 1;

Qy 18 CTCGCTATCGTCAGAGTCGGCGCGCGAGCTGTCATCTCGTCATCGTCAGTCGGCGG 77
Db 160 CTACTCTCTTGTTGGTAACCTCAAGAGTGGCGCTGTGCTGGTGTCTCTCGCGCG 101
Qy 78 CCGCGACTCGACGATGAGGAGATGACGAGT-----CCGCGCGCGCGACTCGACGATGA 132
Db 100 TGCCTACTACCCGATGAGAGATGACAGCTGCGCGAGGGCTTCGATGAGCCGCTCA 41
Qy 133 GCGAGATGACCACTCCGCGCG 154
Db 40 GCGCATGCGCCAGCGCGCGCG 19

RESULT 39
US-10-753-646-15
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
; FILE REFERENCE: 5940. US. P3
; CURRENT APPLICATION NUMBER: US/10/753,646
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/08/924,287A
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 08/851,350
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synV2
; US-10-753-646-15

Query Match 15.7%; Score 24.2; DB 18; Length 175;
Best Local Similarity 62.3%; Pred. No. 5.1e+02;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 15 CATCTGCTATCGTCAGAGTCGGCGCGAGCTGTCATCTGCTATCGTCAGTCGG 74
Db 31 CATCAGCTGTGTCTGTGTCGCGCGCGAGCTGAAGAGCTGACTCACTTCGCGTGG 90
Qy 75 C 75
Db 91 C 91

RESULT 40
US-10-753-646-15/c
; Sequence 15, Application US/10753646
; Publication No. US20040138127A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS FOR INHIBITING
; FILE REFERENCE: 5940. US. P3
; CURRENT APPLICATION NUMBER: US/10/753,646
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US/08/924,287A
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: US 08/851,350
; PRIOR FILING DATE: 1997-05-05
; PRIOR APPLICATION NUMBER: US 08/832,087
; PRIOR FILING DATE: 1997-04-03
; PRIOR APPLICATION NUMBER: US 08/643,219
; PRIOR FILING DATE: 1996-05-03
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 175
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic DNA Fragment synV2
; US-10-753-646-15

Query Match 15.7%; Score 24.2; DB 18; Length 175;
Best Local Similarity 62.3%; Pred. No. 5.1e+02;
Matches 38; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
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```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(183)
;

```

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHITA, TADAO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHARA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,765
CURRENT FILING DATE: 2002-05-29

```

; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(183)
;

```

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHITA, TADAO
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHARA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,765
CURRENT FILING DATE: 2002-05-29


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? PRIOR APPLICATION NUMBER:JP 2001-204089
? PRIOR FILING DATE: 2001-05-30
? PRIOR APPLICATION NUMBER: JP 2001-272657
? PRIOR FILING DATE: 2001-08-02
? NUMBER OF SEQ ID NOS: 15109
? SEQ ID NO 3130
? LENGTH: 192
?
? TYPE: DNA
?
? ORGANISM: Streptomyces avermitilis
?
? FEATURE:
?
? NAME/KEY: CDS
? LOCATION: (1)..(192)
US-10-156-761-3130

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Query Match	15.3%	Score 23.6	DB 15	Length 192
Best Local Similarity	64.8%	Pred. No. 7.7e+02		
Matches 35; Conservative	0	Mismatches 19	Indels 0	Gaps 0

Oy 48 TGTGATCTCGCTCATCTGTCGAATGGGCGGCCCACTGCAGATGAGCCAGA 101
 ||||| ||||| ||||| ||||| |||||
Db 157 TCGTCACTCATTGATGATCGGGGCGACGCTCGAAGACGCGAGATAGAACCCGA 104

RESULT 45

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US-10-425-115-22757
: Sequence 22757, Application US/10425115
: Publication No. US20040214272A1
: GENERAL INFORMATION:
: APPLICANT: La Rosa, Thomas J.
: APPLICANT: Kovacic, David K.
: APPLICANT: Zhou, Yihua
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
: TITLE OF INVENTION: Plants
: FILE REFERENCE: 38-21(53222)B
: CURRENT APPLICATION NUMBER: US/10/425,115
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 369326
: SEQ ID NO 22757
: LENGTH: 155
: TYPE: DNA
: ORGANISM: Zea mays
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(155)
: OTHER INFORMATION: unsure at all n locations
: FEATURE:
: OTHER INFORMATION: Clone ID: MRT4577_120756C.1
US-10-425-115-22757

```

Query Match	15.2%	Score 23.4	DB 18	Length 155
Best Local Similarity	50.0%	Pred. No. 8.9e+02		
Matches 42; Conservative	0	Mismatches 42	Indels 0	Gaps 0

Qy 63 TCGTGAGTGGCGGCGCCCACTCGACGATGACGCGATGACCAAGTCCGGCGCCGAC 122
Db 57 TCGTGACCGGGGGCGGCGAAGCNCNNCACTAAGNTTCAACTCCNNCCGNTGAA 116

QY 123 TCGACGATGAGCGAGATGACCAGC 146
1.17 GCGACAGNGCCGAAGCGAGGAAC 140
Db

Search completed: April 9, 2005, 02:42:41
Job time : 498 secs

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RESULT 1
US-09-313-294A-6653

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Sequence 6653, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PJ-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ. ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6653
LENGTH: 197
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700352170HL
NAME/KEY: unsure
LOCATION: 108, 196
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6653

```

Query Match	18.2%	Score 28;	DB 4;	Length 197;
Best Local Similarity	51.2%	Pred. No. 2e+02;		
Matches	64;	Conservative	0;	Mismatches 61;
				Indels 0;
				Gaps 0;

Oy 28 GTCAAGTCGGGCGGCGGAGCTGTATCTCGCTCATCTCAAGTCGGGCGGCGGCGGATC 87
 Db 63 GGGCGGGTGTCCGCCCGATCTGCTTGCCCGACAGCTGTAACTCTCTCAAGTCTC 122
 Oy 88 GACATATAGGAGATATACCAAGCTCGGCGGCGGCGGATCTCGACGATGACGAGTCAAGT 147
 Db 123 AGTCAGGAGCAAGATGTGTGTCCGGCGGCGAGATGACCGAAGAGCCGGAGAAACAGGA 182
 Oy 148 CCGGC 152
 Db 183 GCAAGC 187

US-09-313-294A-6653/c
; Sequence 6653, Application US/09313294A

```

/ GENERAL INFORMATION:
/ APPLICANT: Laljudi, Raghunath V.
/ APPLICANT: Ito, Laura Y.
/ APPLICANT: Sherman, Bradley K.
/ TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EARS
/ FILE REFERENCE: PI-0017 US
/ CURRENT APPLICATION NUMBER: US/09/313,294A
/ CURRENT FILING DATE: 1999-05-14
/ NUMBER OF SEQ ID NOS: 7600
/ SOFTWARE: PERL Program
/ SEQ ID NO 6653

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/ ORGANISM: Zea mays
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: incyte ID No. 6476212 700352170H1
/ NAME/KEY: unsure
/ LOCATION: 108, 196
/ OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-6653

```

Query Match	18.2%	Score 28;	DB 4;	Length 197;
Best Local Similarity	51.2%;	Pred. No. 2e+03;		
Matches 64;	Conservative 0;	Mismatches 61;	Indels 0;	Gaps 0;

QY 3 GCGGAGCTGGTATCTGGCTCATCGTCGAGTCGGCGGCGGAGCTGGTCAATCTCGCTCA 62

Db 187 GCGGCTCTGGCTTCTCCGCGCTCTCTCTCGGTATCTCTGCGGACACCACTTTGGCTCC 122

QY 63 TCGGCGAGTCGGCGGCGCGCGGACATCGACGATGAGCGAGATGACAGCTTCGGCGCGCGAC 122

Db 127 TGACTGAGACTGGAGGAGANGTAAACAGCTGCTCGGGCGAAGCAGATCGGGCGGACACC 68

QY 123 TCGAC 127

Db 67 GCGGC 63

US-09-513-999C-13979
; Sequence 13979, Application US/09513999C

```

/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Duclert, A.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
/ Patent No. 6783361
/ FILE REFERENCE: 59.US2.REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681

```

```
SOFTWARE: Patentc.pml
SEQ ID NO 13979
LENGTH: 195
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```

? ORGANISM: Homo sapiens
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 9
? OTHER INFORMATION: s=g or c
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 11
? OTHER INFORMATION: n=a, g, c or t
?
? FEATURE:
? NAME/KEY: misc_feature
? LOCATION: 57
? OTHER INFORMATION: r=a or g
?
US-09-03-999C-13979

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Query Match	17.3%	Score 26.6;	DB 4;	length 195;
Best Local Similarity	56.2%	Pred. No. 4.5e+02;		
Matches 50; Conservative	0;	Mismatches 39;	Indels 0;	Gaps 0;

QY 3 GGGGCCGACCTGTATATCTCGCTATCGTCAAGTCGAGGCGGCGCGCACTCGAAGATGAG 96

Db 46 GCTGGCGGCGRGTCGTCTGCGCTTCGGCGGAGATTCTTTCGCTCCGCGCTGGGCTAGGT 105

QY 97 CGAGATGACCAAGCTCGGGCCGCCGACTCG 125

Db 106 CTACGTCCCAAGCTTCAGCGCGCGGCTCG 134

US-09-513-999C-13979/c
; Sequence 13979, Application US/09513999C

```

; Patent No. 6783961
;
; GENERAL INFORMATION:
;
; APPLICANT: Dumas Milne Edwards, J.B.
;
; APPLICANT: Duclert, A.

```

```

/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
/ Patent No. 6783961
/ FILE REFERENCE: 59, US2, REG
/ CURRENT APPLICATION NUMBER: US/09/513,999C
/ CURRENT FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/122,487
/ PRIOR FILING DATE: 1999-02-26
/ NUMBER OF SEQ ID NOS: 36681
/ SOFTWARE: Patent.pm
/ SEQ ID NO 13979
/ LENGTH: 195
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 9
/ OTHER INFORMATION: s=g or c
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 11
/ OTHER INFORMATION: n=a, g, c or t
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 57
/ OTHER INFORMATION: r=a or g
/ US-09-513-999C-13979

```

Query Match	17.3%	Score	26.6	DB	4	Length	195
Best Local	56.2%	Pred.	No. 4.5e+02				
Matches	50	Conservative	0	Mismatches	39	Indels	0
						Gaps	0

[illegible]

```

RESULT 5
US-09-621-976-19276
Sequence 19276: Application US/09621976
Patent NO. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins
FILE REFERENCE: GENEST 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent .pm
SEQ ID NO 19276
LENGTH: 171
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-19276

```

Query Match	17.0%	Score 26.2	DB 4	Length 171
Best Local Similarity	55.1%	Pred. No. 5.7e+02		
Matches 49	Conservative 1	Mismatches 39	Indels 0	Gaps 0

Dy 37 GCGGCGGAGCTGGTATCTGGCTATTCGTCAAGTCGGCGGCCGCACTGCACGATAAG 96
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 47 GCTGCGCGCGGTTGTTCTCCGCTTCGGCGGAATTCTCTTCGCTCCGGCTCCGACTTAGGT 108

QY 97 CGAGATGACCCAGCTCCGGCGGCCGACTCG 123
| | | | | : ||
Db 107 CTACGTCCCAGCTCCAGCGCGCGMTCG 135

```

RESULT 6
US-09-621-976-19276/c
; Sequence 19276, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 19276
; LENGTH: 171
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-19276

```

Query Match 17.0%; Score 26.2; DB 4; Length 171;
Best Local Similarity 55.1%; Pred. No. 5.7e+02;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Dy 30 CGAGTCCGGCGGCGGAGACTGTGCATCTCCTCATCTCGATCGAGTCGGCGGGCGCCGCAATTCCA 89
| | | | | | | | | | | | | | | | | | | | | |
Db 135 CGAACCGGGCGGCTGGAGCTGGGGACGTAAACCTTAAGGCCGAGCGCAGAGGAAAAATCC 76
| | | | | | | | | | | | | | | | | | | | | |
Dy 90 CGATGACCGAGATGACCAGTCCGGCGGC 118
| | | | | | | | | | | | | | | | | | | | | |
Db 75 CGCCGAACGAGACACCGCGCCGCGAGC 47
| | | | | | | | | | | | | | | | | | | | | |

RESULT 7
 US-08-952-670-3
 Sequence 3, Application US/08952670
 Patent No. 6117636
 GENERAL INFORMATION:
 APPLICANT: Taddel, Emmanuelle
 APPLICANT: Aufere, Robert
 TITLE OF INVENTION: METHOD FOR DETECTING HEAT-RESISTANT
 TITLE OF INVENTION: MICRO-ORGANISMS CAPABLE OF CONTAMINATING CERTAIN FOOD
 TITLE OF INVENTION: PRODUCTS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/952,670
 FILING DATE: 09-MAR-1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR96/00821
 FILING DATE: 31-MAY-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 95/06578
 FILING DATE: 02-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Granados, Patricia D.
 REGISTRATION NUMBER: 33,683
 REFERENCE/DOCKET NUMBER: 065691/0128
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)672-5300


```

?
? EARLIER APPLICATION NUMBER: 09/007,005
? EARLIER FILING DATE: 1998-01-14
? NUMBER OF SEQ ID NOS: 38
? SOFTWARE: Paetsted for Windows Version 4.0
? SEQ ID NO 34
? LENGTH: 123
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURES:
? OTHER INFORMATION: n = a, g, t, or c. s = c or g
US-09-247-190-34

```

Query Match	16.2%	Score 25;	DB 3;	Length 123;
Best Local Similarity	15.0%	Pred. No. 1.1e+03;		
Matches	16;	Conservative	65;	Indels 0;
		Mismatches	65;	Gaps 0

[illegible]

```

RESULT 11
US-09-513-999C-16612
; Sequence 16612, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J. B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J. Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 16612
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-513-999C-16612

```

Query Match	16.1%	Score 24.8	DB	Length 181
Best Local Similarity	67.3%	Pred. No. 1,3e+03		
Matches	35	Conservative	0	Mismatches 17
				Indels 0
				Gaps 0
QY	25	ATCGTCAGTGGCGCGCCGAGACTGCTATCTCGTCAATCGTCAGTGGCG	76	
Db	20	ATCCCTTACTTGGCGCGCGCGAGGGGCTCTGCGCTTCGCGGGGCGCG	71	

```

RESULT 12
US-09-513-999C-16612/C
; Sequence 16612, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681

```

```

; SOFTWARE: Patent.pm
; SEQ ID NO 16612
; LENGTH: 181
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-16612

```

Query Match	16.1%	Score 24.8;	DB 4;	Length 181;
Best Local Similarity	67.3%;	Pred. No. 1.3e+03;		
Matches 35;	Conservative 0;	Mismatches 17;	Indels 0;	Gaps 0;

Dy 79 CGCCGACTTCAGCATTAGCGCATGACCACTCCGGCCGCCACTCGACGAT 130
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 CGCCGCCCGCGAAGACCAGCGCTTGC GCCGCCCGCAGAGTAGGGGAT 20

US-08-651-350-15
US-08-651-350-15
Sequence 15, Application US/08851350
Patent No. 6057122

GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTITUMORGENIC PEPTIDES,
POLYNUCLEOTIDES ENCODING SAME AND METHODS
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME AND METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,350
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Diane
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US.P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-5137
TELEFAX: 847-938-2623
TELEX:

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
.LENGTH: 175 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-651-350-15

	Query Match	15.7%	Score 24.2	DB 3	Length 175;		
	Best Local Similarity	62.3%	Pred. No. 1.6e+03;				
	Matches	38;	Conservative	0; Mismatches	23; Indels	0; Gaps	0;
OY	15	CATTCGCTCATCGTGCAGTCCGGCGGACGTGTCATCTGCGTATCGAGTCG	74				
Dδ	31	CATTACGGTGTTGCTGTGTCGCCGCGGACGTGAAGAAGCTGGCTCACTTCGGGTGG	90				
OY	75	C	75				
Dδ	91	C	91				

Query Match	15.3%	Score 23.6	DB 4	Length 71
Best Local Similarity	62.5%	Pred. No. 2.4e+03		
Matches	35	Conservative 1	Mismatches 20	Indels 0
				Gaps 0

Qy	73	GGCGCGCCGACATCGACGATGAGCGAGATGACGACTTCGCGCGCCGACCTGACG	128
Db	8	GGCGCGCGCCGAGGTGAGCGCGCGCGCGACGACCCGACGACGAGCGGAGACGAGAG	63

```

RESULT 18
US-09-513-999C-15749/C
; Sequence 15749, Application US/0951399C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclerc, A.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513, 999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15749
; LENGTH: 71
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 35
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 45
; OTHER INFORMATION: s=g or c
; US-09-513-999C-15749
;
Query Match 15.3%; Score 23.6; DB 4; Length 71;
Best Local Similarity 62.5%; Pred. No. 2,4e+03;
Matches 35; Conservative 1; Mismatches 20; Indels 0; Gaps 0;
27 GGTGAGTGGGCGGCGGAGGTGTGTCATCTGCTTCATCGTCGAGTGGGCGGCGGC 82

```

Query Match	Score 23.6; DB 4;	Length 195;
Best Local Similarity	58.6%;	Pred. No.25+03;
Matches	41; Conservative	0; Mismatches 29; Indels 0; Gaps 0;
QY	9 GCTGATATCTCGCTCATCTGCAAGTGGCGGCGCGAGCTGCTATCTCGCTCATGCG	68
DB	93 GCTGCGGCTCGCGGTTCAGTCAGACGGCGAGCGCGGACCGCGGCGCAAGCGCGCTTCGGCG	152
QY	69 AGTCGGCGGCG 78	
DB	153 GCTCGGCGGCC 162	

```

, RESULT 20
, US-09-902-540-8568/C
, Sequence 8568, Application US/09902540
, Patent No. 6833447
, GENERAL INFORMATION:
, APPLICANT: Goldman, Barry S.
, APPLICANT: Hinkle, Gregory J.
, APPLICANT: Slater, Steven C.
, APPLICANT: Wiegand, Roger C.
, TITLE OR INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
, FILE REFERENCE: 38-10(15849)B
, CURRENT APPLICATION NUMBER: US/09/902,540
, CURRENT FILING DATE: 2001-07-10
, PRIOR APPLICATION NUMBER: 60/217,883
, PRIOR FILING DATE: 2000-07-10
, NUMBER OF SEQ ID NOS: 16825
, SEQ ID NO 8568
, LENGTH: 195
, TYPE: DNA
, ORGANISM: Myxococcus xanthus
, US-09-902-540-8568

```

Query Match	15.3%	Score 23.6	DB 4	Length 195
Best Local Similarity	58.6%	Pred. No. 2.5e+03		
Matches	41	Conservative	0	Mismatches 29
				Indels 0
				Gaps 0
QY	77	GCCTCCCATCTGACGATGACGATATGACGCTCTCCGCGCCGCGCATCTGACGATGACGGA	136	
DB	162	GGCGCCGAGCGCGCGGAGCGCGCTTGGCGCGCATCGCGCCCTCGGATGATGACCGC	103	
QY	137	GATGACCGAGC	146	
DB	102	GACCGCCAGC	93	

RESULT 21

US-09-902-540-2996
Sequence 2996, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIORITY FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2996
LENGTH: 126
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2996

Query Match 15.1%; Score 23.2; DB 4; Length 126;
Best Local Similarity 50.9%; Pred. No. 3.1e+03;
Matches 55; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 46 GCTGTCATCTCGCTCATCTGCTGAGTCCGCGCCGCGCACTCGACGATGACGAGATGAC 105
DB 3 GATGTCACGGTGGCGCATCGCTCCATCTCTCGCCGCGCGCGCTGATGGCGCATCCAGAC 62
QY 106 CAGCTCCGCGCGCGCACTCGACGATGACGAGATGACGAGTCCGCGCC 153
DB 63 GCCGTGACCGTCAACGCGAGATGAGGCCACGCGCAGCTGTGGGC 110

RESULT 22

US-09-902-540-2996/c
Sequence 2996, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
PRIORITY FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2996
LENGTH: 126
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2996

Query Match 15.1%; Score 23.2; DB 4; Length 126;
Best Local Similarity 50.9%; Pred. No. 3.1e+03;
Matches 55; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 2 GCGCGAGCTGATCTCGCTCATCTGCTGAGTCCGCGCGCGAGTGTGATCTGCTC 61
DB 110 GCCACAGCTGCGCGCTGCTCATCTCGCTGAGCGGTGACGGGCGCTGTGATGCC 51
QY 62 ATGCTGAGTGGCGCGCGCGCACTCGACGATGAGCGAGATGACGAC 109
DB 50 ATCAGCGCGCGCGAGAGATGAGGCGATGCGCACCGTGACCATC 3

RESULT 23

US-08-447-985-14

Sequence 14, Application US/08447985
Patent No. 6399861
GENERAL INFORMATION:

APPLICANT: Adams, Thomas R. et al.
TITLE OF INVENTION: Methods and Compositions for the
Production of Stably Transformed, Fertile Monocot Plants
and Cells Thereof

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,985

FILING DATE: 23-May-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/113,561

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: DEKM:055/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: 512/418-3000

TELEFAX: 713/789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 14:

US-08-447-985-14

Query Match 14.7%; Score 22.6; DB 3; Length 185;
Best Local Similarity 55.8%; Pred. No. 4.5e+03;
Matches 43; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 52 CATCTCGCTCATCTGCTGAGTCCGCGCGCGCACTCGACGATGAGCGAGATGACGAGCTC 111
DB 50 CACGCTATGATGCGCTCGTGGCGCACCGCGCTGCTCGCTCCAGGGGCTCAAGTCCAC 109
QY 112 CGGCGCGCGCACTGAGC 128
DB 110 CGCCAGCTCCCGCTCG 126

RESULT 24

US-08-447-985-14/c
Sequence 14, Application US/08447985
Patent No. 6399861
GENERAL INFORMATION:

APPLICANT: Adams, Thomas R. et al.

TITLE OF INVENTION: Methods and Compositions for the

Production of Stably Transformed, Fertile Monocot Plants
and Cells Thereof

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESS: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA

ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,985
FILING DATE: 23-May-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/113,561
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: DEKM:055/PAR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 713/789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-447-985-14
Query Match 14.7%; Score 22.6; DB 3; Length 185;
Best Local Similarity 55.8%; Pred. No. 4.5e+03;
Matches 43; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 27 CGTCGAGTCGGCGCGGCGGAGCTGTCATCTGCTATGCTGAGTGGCGGCGCCGACT 86
DB 126 CGACGGGAGGCTGGCGGTGACTTGAGCCCTGGAGCGAGCGCGCGGTGGCCGACG 67
QY 87 CGACGATGAGCGAATG 103
DB 66 AGGCATCATCAGCGTG 50
RESULT 25
US-08-852-340-14
Sequence 14, Application US/08852340
Patent No. 6803499
GENERAL INFORMATION:
APPLICANT: Adams, Thomas R., et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
PRODUCTION OF STABLY TRANSFORMED, FERTILE MONOCOT PLANTS
TITLE OF INVENTION: AND CELLS THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-May-1997
CLASSIFICATION: 504
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113,561
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DEKM:146/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-852-340-14
Query Match 14.7%; Score 22.6; DB 4; Length 185;
Best Local Similarity 55.8%; Pred. No. 4.5e+03;
Matches 43; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 52 CATCTGCTATGCTGAGTCGGCGGCGGCGGACTGAGCATGAGCGATGACCACTC 111
DB 50 CACCTATATGAGCTCTGCTCGGCGACCGCGCTGCTCCGTTCCAGGGGCTCAAGTCAC 109
QY 112 CGGCGCGGCGACTCGACG 128
DB 110 CGCAGCGCTCCCGCTG 126
RESULT 26
US-08-852-340-14/c
Sequence 14, Application US/08852340
Patent No. 6803499
GENERAL INFORMATION:
APPLICANT: Adams, Thomas R., et al.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
PRODUCTION OF STABLY TRANSFORMED, FERTILE MONOCOT PLANTS
TITLE OF INVENTION: AND CELLS THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: U.S.
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,340
FILING DATE: 07-May-1997
CLASSIFICATION: 504
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/113,561
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: DEKM:146/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-852-340-14
Query Match 14.7%; Score 22.6; DB 4; Length 185;
Best Local Similarity 55.8%; Pred. No. 4.5e+03;

RESULT 32
US-09-122-399-9/c
Sequence 9, Application US/09122399
Patent No. 6329574
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihaara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Moessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,399
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Moessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-122-399-9

Query Match 14.7%; Score 22.6; DB 3; Length 195;
Best Local Similarity 52.7%; Pred. No. 4.5e+03;
Matches 49; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 27 CGTCGAGCGCGCGCGCGAGTCGTCATCGTCATCGTCGAGTCGCGCGCGCGCGACT 86
Db 136 CGACGGGAGGCTGGCGGTGACCTTGAGACGAGCGAGCGGCGGTGCGCGAGC 77

Qy 87 CGACGATGAGCGAGATGACCGAGCTCCGCGCGCC 119
Db 76 AGGCCATCATCAGCGTTTCATCAGCGTGGCGGCC 44

RESULT 33
US-08-440-646A-9
Sequence 9, Application US/08440646A
Patent No. 6777589
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihaara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Moessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,646A
FILING DATE: 15-May-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/112,245
FILING DATE: 25-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Moessner, Warren D.
REGISTRATION NUMBER: 30,440
REFERENCE/DOCKET NUMBER: 950.13US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 195 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-440-646A-9

Query Match 14.7%; Score 22.6; DB 4; Length 195;
Best Local Similarity 52.7%; Pred. No. 4.5e+03;
Matches 49; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 36 GCGGCGCGGAGCTGTCATCGTCATCGTCGAGTCGCGCGCGCGCGCGACTGACGATGA 95
Db 44 GCGGCGCGGAGCTGTCATCGTCATCGTCGAGTCGCGCGCGCGCGCGACTGACG 103

Qy 96 GCGAGATGACCGAGCTCCGCGCGCGCGACTCGAGC 128
Db 104 AGGGGCTCAGTCACCGCCGACGCTCCCGCTCG 136

RESULT 34
US-08-440-646A-9/c
Sequence 9, Application US/08440646A
Patent No. 6777589
GENERAL INFORMATION:
APPLICANT: Lundquist, Ronald C.
APPLICANT: Walters, David A.
APPLICANT: Kirihaara, Julie A.
TITLE OF INVENTION: Methods and Compositions for the
TITLE OF INVENTION: Production of Stably Transformed, Fertile Monocot Plants
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Moessner, P.A.
STREET: 3500 IDS Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/440,646A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/112,245
; FILING DATE: 25-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Woessner, Warren D.
; REGISTRATION NUMBER: 30,440
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-339-0331
; TELEFAX: 612-339-3061
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-08-440-646A-9

Query Match          14.7%; Score 22.6; DB 4; Length 195;
Best Local Similarity 52.7%; Pred. No. 4.5e+03;
Matches 49; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 27 GGTGATCGGCGCGCGAGCTGTCATCTGTCATCTGAGTCCGCGCCGCACT 86
Db 136 CGAGCGGAGGCTGCGCGTGAAGCCCTCGAAGGAGCGAGCGCGGTGCGCAGC 77
Qy 87 CGACGATGAGCGAGATGACGACGCTCCGCGCC 119
Db 76 AGGCCATCATCAGCGTTCATCAGCGTGGCGCC 44

RESULT 35
US-08-105-168B-6
; Sequence 6, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL:
; ANTI-SENSE:
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium intracellulare
; STRAIN:
; INDIVIDUAL ISOLATE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; FEATURE:
; NAME/KEY:
; LOCATION: 518-717
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-08-105-168B-6

Query Match          14.7%; Score 22.6; DB 1; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

Qy 9 GCTGATCATCTCGCTCATCTCGTCGAGTGGGCGCGGAGCTGTCATCTGTCATCTCG 68
Db 70 GCTGAGTCTCAAGGCGCGCATCGAAGAGCCGTG-GAAGAGTACGAGACCTGCTCA 128
Qy 69 AGTCGGCGCGCGCGCACTCGACGATGAGCGAGATGACGACTCCG 113
Db 129 AGTCGGCAAGAGAGTGTGAGACCAAGACCAAGATCGCTGCACCG 173
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RESULT 36
US-08-105-168B-6/c
; Sequence 6, Application US/08105168B
; Patent No. 5589585
; GENERAL INFORMATION:
; APPLICANT: MABILAT et al.
; TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION
; TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET
; TITLE OF INVENTION: MYCOBACTERIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oliff & Berridge
; STREET: 700 South Washington Street, Suite 300
; CITY: Alexandria,
; STATE: Virginia
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" DS/HD
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS DOS 3.1
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1993
; APPLICATION NUMBER: US/08/105,168B
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR9210094
; FILING DATE: August 8, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: William P. Berridge
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 28835
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
```

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-105-168B-6

Query Match 14.7%; Score 22.6; DB 1; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 42 CGAGCTGTCATCTGCTCATGTCGAGTCGGCGCCGCGACTCGACGATGAGCGAGA 101
DB 173 CGGTGGCAGCGATCTGTGCTTGTGCTGACCTCTTGCGCGACTTGAGCGGGTCTCGG 114
QY 102 TGACCACTCCGCGCCGCGACTCGACGATGAGCGAGATGACGAGC 146
DB 113 TGACCTTCT-CGACGCGCTTCTGATGCGCGCTTGAGACCCAGC 70

RESULT 37

US-08-698-948-6
Sequence 6, Application US/08698948
Patent No. 5849901

GENERAL INFORMATION:
APPLICANT: MABILIAT et al.

TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DET

TITLE OF INVENTION: MYCOBACTERIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge

STREET: 700 South Washington Street, Suite 300

CITY: Alexandria,

STATE: Virginia

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" DS/HD

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS 3.1

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/698,948

FILING DATE: August 16, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/105,168

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR9210094

FILING DATE: August 8, 1992

ATTORNEY/AGENT INFORMATION:

NAME: William P. Berridge

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28835A

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 200 base pairs

TYPE: nucleic acid

STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-6

Query Match 14.7%; Score 22.6; DB 2; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 9 GCTGTCATCTGCTCATGTCGAGTCGGCGCCGAGCTGTGTCATCTGCTCATCTGCTCG 68
DB 70 GCTGGTCTCAAGCGCGCGCATCGAAGGCCGTC-GAAGAGTCAACGAGACCTGCTCA 128
QY 69 AGTCGGGGCGCCCGCGACTCGACGATGAGCGAGATGACCACTCGG 113
DB 129 AGTCGGCCAAAGAGTGAAGCAAGACCAAGATGCTGCAACCG 173

RESULT 38

US-08-698-948-6/c
Sequence 6, Application US/08698948
Patent No. 5849901

GENERAL INFORMATION:
APPLICANT: MABILIAT et al.

TITLE OF INVENTION: DNA FRAGMENTS OF MYCOBACTERIA, AMPLIFICATION

TITLE OF INVENTION: PRIMERS, HYBRIDIZATION PROBES, REAGENTS AND METHOD FOR THE DETI

TITLE OF INVENTION: MYCOBACTERIA

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Oliff & Berridge

STREET: 700 South Washington Street, Suite 300

CITY: Alexandria,

STATE: Virginia

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" DS/HD

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS 3.1

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/698,948

FILING DATE: August 16, 1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/105,168

FILING DATE: August 12, 1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR9210094

FILING DATE: August 8, 1992

ATTORNEY/AGENT INFORMATION:

NAME: William P. Berridge

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 28835A

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 200 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
STRANDEDNESS: single-stranded
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL:
ANTI-SENSE:
ORIGINAL SOURCE:
ORGANISM: Mycobacterium intracellulare
STRAIN:
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
FEATURE:
NAME/KEY:
LOCATION: 518-717
IDENTIFICATION METHOD:
OTHER INFORMATION:
US-08-698-948-6

Query Match 14.7%; Score 22.6; DB 2; Length 200;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;

Matches 60; Conservative 0; Mismatches 44; Indels 1; Gaps 1;

QY 42 CGGAGCTGTCATCTCGCTCATCGTCGAGTCGCGCGCGCGGACCTCGACGATGAGCGAGA 101
DB 173 CGGTGGCAGCATGTGCTCTTGCTCTGACCTCTTGCGGACCTTGAGCGAGGCTCTCG 114
QY 102 TGACCACTCCGCGCGCGGACCTCGACGATGAGCGAGTACACAGC 146
DB 113 TGACCTTCT-CGACGCGCTTCTCGATGCGCGCTTGAGACCCAGC 70

RESULT 39

US-09-902-540-8045

; Sequence 8045, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 8045

; LENGTH: 174

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-8045

Query Match 14.5%; Score 22.4; DB 4; Length 174;
Best Local Similarity 59.4%; Pred. No. 5e+03;

Matches 36; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 40 GCCGAGCTGTCATCTCGCTCATCTGATCGGCGCGCGCGGACCTCGACGATGAGCGAGA 99
DB 99 GCGCGCGCGCGCGCGCTCGGATTCGGGAGCTCGACGCGCGCGCTTACGAGAGGCGCTGCT 158
QY 100 GATG 103
DB 159 GAAG 162

RESULT 40

US-09-902-540-8045/C

; Sequence 8045, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8045
; LENGTH: 174
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8045

Query Match 14.5%; Score 22.4; DB 4; Length 174;
Best Local Similarity 59.4%; Pred. No. 5e+03;

Matches 36; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 52 CATCTGCTCATCTCGATCTGAGTCGCGCGCGGACCTCGACGATGAGCGAGTACACAGC 111
DB 162 CTTGACGAGCGCTTCTCTGTAAGCGGCTCGACCTCGCGGATACGAGCGCGCGCGCG 103
QY 112 CGGC 115
DB 102 CGGC 99

RESULT 41

US-09-902-540-7303

; Sequence 7303, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Wiegand, Roger C.

; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

; FILE REFERENCE: 38-10(15849)B

; CURRENT APPLICATION NUMBER: US/09/902,540

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 16825

; SEQ ID NO 7303

; LENGTH: 102

; TYPE: DNA

; ORGANISM: Myxococcus xanthus

US-09-902-540-7303

Query Match 14.3%; Score 22; DB 4; Length 102;
Best Local Similarity 57.1%; Pred. No. 6.1e+03;

Matches 40; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTGCTCATCTGATCGGCGCGCGGACCTCGACGATGAGCGAGT 60
DB 6 CTGCGGAGCGCTTCTCTGTAATCTGAGGCGCTGCGCGCGCGCGCTGATGAGCGCC 65
QY 61 CATGTCGAG 70
DB 66 CGAGTGGCG 75

RESULT 42

US-09-902-540-7303/C

; Sequence 7303, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

Search completed: April 9, 2005, 02:34:14
Job time : 133 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:27:07 ; Search time 424 Seconds
(without alignments)
2150.095 Million cell updates/sec

Title: US-09-887-194a-13

Perfect score: 154
Sequence: 1 cggccgcgagctgcgtcatctc.....gagatgaccagctccgcccgcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4887668

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : N Geneseq 16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	154	6	AAD29231 Plasmids
2	154	100.0	154	6	AAD29231 Plasmids
3	154	100.0	154	6	AAD32908 Plasmids
4	154	100.0	154	6	AAD32908 Plasmids
5	154	100.0	154	12	ADQ07968 Seed spec
6	154	100.0	154	12	ADQ07968 Seed spec
7	81	52.6	81	6	ABK10711 Artificialia
8	81	52.6	81	6	ABK10711 Artificialia
9	80	51.9	80	6	AAD29230 Plasmids
10	80	51.9	80	6	AAD29230 Plasmids
11	80	51.9	80	6	AAD32907 Plasmids
12	80	51.9	80	6	AAD32907 Plasmids
13	80	51.9	92	6	ABK10712 Artificialia
14	80	51.9	92	6	ABK10712 Artificialia
15	80	51.9	92	6	AAD29232 ELVSLIVE
16	80	51.9	92	6	AAD29232 ELVSLIVE
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18	44	28.6	44	6	ABK10710 Artificialia
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24	26.6	17.3	156	6	AAL44709	Aal44709 Human glu
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26	26.6	17.3	190	6	AAL44706	Aal44706 Human glu
27	26.6	17.3	195	3	AAC09904	Aac09904 Human sec
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30	26	16.9	170	4	AAL17387	Aal17387 Human bre
31	26	16.9	189	4	AAL09498	Aal09498 Human bre
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34	25.6	16.6	183	2	AAT49353	Aat49353 N. fische
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36	25	16.2	123	3	AAA94339	Aaa94339 123-mer D
37	24.8	16.1	108	12	ACH88658	Ach88658 Human gen
38	24.8	16.1	108	12	ACH88658	Ach88658 Human gen
39	24.8	16.1	130	10	ACD96616	AcD96616 Human col
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43	24.4	15.8	164	7	ADS69652	AdS69652 Corn seed
44	24.4	15.8	164	7	ADS69652	AdS69652 Corn seed
45	24.4	15.8	185	4	AAI27481	Aai27481 Probe #17
46	24.4	15.8	185	4	AAI27481	Aai27481 Probe #17
47	24.4	15.8	185	4	ABA75795	AbA75795 Human foe
48	24.4	15.8	185	4	ABA75795	AbA75795 Human foe
49	24.4	15.8	185	4	AAI56451	Aai56451 Probe #25
50	24.4	15.8	185	4	AAI56451	Aai56451 Probe #25
51	24.4	15.8	185	4	ABA40366	AbA40366 Probe #18
52	24.4	15.8	185	4	ABA40366	AbA40366 Probe #18
53	24.4	15.8	185	4	AAK50468	Aak50468 Human bon
54	24.4	15.8	185	4	AAK50468	Aak50468 Human bon
55	24.4	15.8	185	4	AAK24480	Aak24480 Human bra
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57	24.4	15.8	185	4	ABS50091	AbS50091 Human liv
58	24.4	15.8	185	4	ABS50091	AbS50091 Human liv
59	24.4	15.8	185	6	ABS23940	AbS23940 Human gen
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61	24.2	15.7	175	2	AAT93196	Aat93196 Synthetic
62	24.2	15.7	175	2	AAT93196	Aat93196 Synthetic
63	24.2	15.7	175	3	AAA52287	Aaa52287 Synthetic
64	24.2	15.7	175	3	AAA52287	Aaa52287 Synthetic
65	24.2	15.7	175	12	ADR23668	AdR23668 Synthetic
66	24.2	15.7	175	12	ADR23668	AdR23668 Synthetic
67	24.2	15.7	175	12	ADQ28293	AdQ28293 Abbott-mo
68	24.2	15.7	175	12	ADQ28293	AdQ28293 Abbott-mo
69	23.6	15.3	71	3	AAC11674	Aac11674 Human sec
70	23.6	15.3	71	3	AAC11674	Aac11674 Human sec
71	23.6	15.3	178	10	ACD93885	AcD93885 Human col
72	23.6	15.3	178	10	ACD93885	AcD93885 Human col
73	23.4	15.2	121	12	ADL80636	AdL80636 Human rec
74	23.4	15.2	121	12	ADL80636	AdL80636 Human rec
75	23.2	15.1	132	9	ADA49202	Ada49202 Maize gen
76	23.2	15.1	132	9	ADA49202	Ada49202 Maize gen
77	23.2	15.1	192	6	ABK44945	AbK44945 CDNA enco
78	23.2	15.1	192	6	ABK44945	AbK44945 CDNA enco
79	23	14.9	74	4	AAF58508	Aaf58508 Nucleotid
80	23	14.9	74	4	AAF58508	Aaf58508 Nucleotid
81	23	14.9	74	10	ADP17445	AdP17445 Il-1 rece
82	23	14.9	74	10	ADP17445	AdP17445 Il-1 rece
83	23	14.9	74	10	ADF53650	AdF53650 Phosphata
84	23	14.9	74	10	ADF53650	AdF53650 Phosphata
85	23	14.9	74	10	ADP44538	AdP44538 Mouse kin
86	23	14.9	74	10	ADP44538	AdP44538 Mouse kin
87	23	14.9	74	10	ADF74728	AdF74728 Synthetic
88	23	14.9	74	10	ADF74728	AdF74728 Synthetic
89	23	14.9	74	12	ADBS2664	AdBS2664 Oligonuci
90	23	14.9	74	12	ADBS2664	AdBS2664 Oligonuci
91	23	14.9	74	12	ADFS0664	AdFS0664 Sequenci
92	23	14.9	74	12	ADFS0664	AdFS0664 Sequenci
93	23	14.9	74	12	ADG31227	AdG31227 Novel mou

C 94	23	14.9	74	12	ADG31227	Adg31227	Novel mouse
C 95	23	14.9	74	12	ADK6E195	Adk6e195	Mouse 1am
C 96	23	14.9	74	12	ADK6E195	Adk6e195	Mouse 1am
C 97	23	14.9	176	6	ABK16750	Abk16750	Human cDN
C 98	23	14.9	176	6	ABK16750	Abk16750	Human cDN
C 99	23	14.9	192	6	ABQ91010	Abq91010	M. capsuli
C 100	23	14.9	192	6	ABQ91010	Abq91010	M. capsuli

ALIGNMENTS

```

RESULT 1
AADD29231
ID      AAD29231 standard; DNA; 154 BP.
XX
XX
XX
AAD29231;
DT      07-MAY-2002 (first entry)
XX
XX
Plasmids pKS13 2X ELVISLIVES complementary repeat DNA.
XX
XX
Recombinant construct; gene expression; plasmid pKS13; ds
XX
XX
Unidentified.
XX

```

PH	Key	Location/Qualifiers
FT	CDS	7..36
FT		/tag= a
FT		/product= "ELVISLIVES protein"
FT	CDS	44..74
FT		/tag= b
FT		/product= "ELVISLIVES protein"
FT	CDS	complement(82..111)
FT		/tag= c
FT		/product= "ELVISLIVES protein"
FT	CDS	complement(119..148)
FT		/tag= d
FT		/product= "ELVISLIVES protein"
PPN	WO200200904-A2.	
PPD	03-JAN-2002.	
PPF	22-JUN-2001; 2001WO-US019962.	
PPR	23-JUN-2000; 2000US-0213961P.	
PPA	(DUPO) DU PONT DE NEMOURS & CO E. I.	
PPA	(PION-) PIONEER HI-BRED INT INC.	
PP1	Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,	
PP1	Nichols SE;	
PPR	WPI; 2002-139927/18.	
PPR	P-PSDB; AAE18333.	
PPT	New recombinant construct having a promoter operably linked to a DNA	
PPT	sequence which when expressed produces an RNA having homology to a target	
PPT	mRNA and its reverse complement unrelated to endogenous DNA, for reducing	
PPT	gene expression.	
PPX	Claim 45; Page 37; 77pp; English.	
PPX	The present invention relates to a new recombinant construct. The	
PPX	construct comprises a promoter operably linked to a DNA sequence which	
PPX	when expressed by a host produces an RNA having homology to at least one	
PPX	target mRNA expressed by the host and complementary RNA regions. The	
PPX	recombinant construct is useful for reducing the expression of a target	
PPX	mRNA or any similar endogenous mRNA. The RNAs expressed from the	
PPX	recombinant constructs are also used in reducing expression of a target	
PPX	mRNA or any similar endogenous mRNA. The sequences and their reverse	
PPX	complements can be used to reduce the expression of any endogenous	

CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC 11. The present sequence is 2X ELVISIVIS complementary repeat region DNA
CC found in plasmid pKS133 used in the exemplification of the invention
XX
50 Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match	100.0%;	Score 154;	DB 6;	Length 154;
Best Local Similarity	100.0%;	Pred. No. 2.7e-28;		
Matches 154;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy	1	CGGCGGAGGTGGTATCTCGCTCATCTCGAGTGGGGCGGAGCGGAGTCTGGCT	60
Db	1	CGGCGGAGGTGGTATCTCGCTCATCTCGAGTGGGGCGGAGCGGAGTCTGGCT	60
Qy	61	CATCTCGAGTGGGGCGGCGCGGACTTGCAGATGAGCAATGACMACTTCGGCGCGG	120
Db	61	CATCTCGAGTGGGGCGGCGCGGACTTGCAGATGAGCAATGACMACTTCGGCGCGG	120
Qy	61	CATCTCGAGTGGGGCGGCGCGGACTTGCAGATGAGCAATGACMACTTCGGCGCGG	120
Db	61	CATCTCGAGTGGGGCGGCGCGGACTTGCAGATGAGCAATGACMACTTCGGCGCGG	120
Qy	121	ACTCGACATGAGCGAGATGACCAAGCTTCGGCGG	154
Db	121	ACTCGACATGAGCGAGATGACCAAGCTTCGGCGG	154
Qy	121	ACTCGACATGAGCGAGATGACCAAGCTTCGGCGG	154
Db	121	ACTCGACATGAGCGAGATGACCAAGCTTCGGCGG	154

	RESULT 2
ID	AAD29231/C
AC	AAD29231 standard; DNA; 154 BP.
D7	AAD29231;
D7T	07-MAY-2002 (first entry)
DE	Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
KM	Recombinant construct; gene expression; plasmid pXS133; ds.
OS	Unidentified.
XX	
FH	Key
FH	CDS
FT	Location/Qualifiers
FT	/tag= a
FT	/product= "ELVISLIVES protein"
FT	44..74
FT	/tag= b
FT	/product= "ELVISLIVES protein"
FT	complement(82..111)
FT	*tag= c
FT	/product= "ELVISLIVES protein"
FT	complement(119..148)
FT	*tag= d
FT	/product= "ELVISLIVES protein"
PN	MO200200904-A2.
PD	03-JAN-2002.
Pf	22-JUN-2001; 2001WO-US019662.
PR	23-JUN-2000; 2000US-0213961P.
PA	(DUPO) DU PONT DE NEMOURS & CO E I.
PA	(PION-) PIONEER HI-BRED INT INC.
PI	Glaesman KP, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI	Nichols SE;
PF	MFI; 2002-139927/18.
PT	New recombinant construct having a promoter operably linked to a DNA
PT	sequence which when expressed produces an RNA having homology to a target
PT	mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT	gene expression.
DR	P-FSDB; AAEI8333.
XX	

XX Claim 45; Page 37; 77pp; English.

PS The present invention relates to a new recombinant construct. The

XX construct comprises a promoter operably linked to a DNA sequence which

CC when expressed by a host produces an RNA having homology to at least one

CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target

CC mRNA or any similar endogenous mRNA. The RNAs expressed from the

CC recombinant constructs are also used in reducing expression of a target

CC mRNA or any similar endogenous mRNA. The sequences and their reverse

CC complements can be used to reduce the expression of any endogenous

CC genomic sequence that shares substantial similarity to nucleic acid

CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA

CC found in plasmid pKS133 used in the exemplification of the invention

XX

XX Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

QQ

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCT 60

DB 154 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCT 95

QY 61 CATGTCGAGTCGCGCGCGCGCGAGTCGAGATGACGATGACGATCGCGCGCGCG 120

DB 94 CATGTCGAGTCGCGCGCGCGCGAGTCGAGATGACGATGACGATCGCGCGCGCG 35

QY 121 ACTGACGATGAGGAGATGACGATGACGATCGCGCGCGCG 154

DB 34 ACTGACGATGAGGAGATGACGATGACGATCGCGCGCG 1

RESULT 3

AAD32908

ID AAD32908 standard; DNA; 154 BP.

XX

XX AAD32908;

AC

XX 01-JUL-2002 (first entry)

DT

XX Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

DE

XX Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KM oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KM de.

XX

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

FH 7..36

FT CDS /*tag= a

FT /*product= "ELVISLIVES protein"

FT 44..74

FT /*tag= b

FT /*product= "ELVISLIVES protein"

FT complement(82..111)

FT /*tag= c

FT /*product= "ELVISLIVES protein"

FT complement(119..148)

FT /*tag= d

FT /*product= "ELVISLIVES protein"

XX

XX WO200216565-A2.

XX

XX 28-FEB-2002.

XX

XX 22-AUG-2001; 2001WO-US026246.

XX

XX 22-AUG-2000; 2000US-0226996P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

PA

XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

XX WPI; 2002-269353/31.

DR P-PSDB; AAE20554.

XX

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,

PT useful in creating transgenic plants having altered levels of mono-, poly

PT - and unsaturated fatty acids and in increasing the unsaturation levels

PT in cellular lipids.

XX

XX Example 9; Page 43; 77pp; English.

PS

XX The present invention relates to diverged delta-9 fatty acid desaturase

CC proteins and polynucleotides encoding such proteins. The nucleic acid

CC sequences may be used to increase the level of unsaturation in cellular

CC lipids, including oil, in tissues when the enzyme is absent or rate-

CC limiting, to isolate cDNAs and genes encoding homologous proteins from

CC the same or other plant species and to create transgenic plants in which

CC cell types or developmental stages in which they are not normally found,

CC thus altering the level of mono-, poly- and unsaturated fatty acids in

CC those cells. They are useful as probes for genetic and physical gene

CC mapping and as markers, e.g. restriction fragment length polymorphism

CC (RFLP) markers. The peptides can be used to immunise animals to produce

CC antibodies specific for the peptides and proteins. The present sequence

CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133

CC This sequence is used in the exemplification of the invention for the

CC suppression of Pad2 in soybean

XX

XX Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

QQ

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCT 60

DB 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCT 60

QY 61 CATGTCGAGTCGCGCGCGCGCGAGTCGAGATGACGATGACGATCGCGCGCGCG 120

DB 61 CATGTCGAGTCGCGCGCGCGCGAGTCGAGATGACGATGACGATCGCGCGCGCG 120

QY 121 ACTGACGATGAGGAGATGACGATGACGATCGCGCGCGCG 154

DB 121 ACTGACGATGAGGAGATGACGATGACGATCGCGCGCG 154

RESULT 4

AAD32908/C

ID AAD32908 standard; DNA; 154 BP.

XX

XX AAD32908;

AC

XX 01-JUL-2002 (first entry)

DT

XX Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

DE

XX Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KM oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KM de.

XX

XX Unidentified.

OS

XX

XX Key Location/Qualifiers

FH 7..36

FT CDS /*tag= a

FT /*product= "ELVISLIVES protein"

FT 44..74

FT /*tag= b

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FT      /product="ELVISLIVES protein"
FT      complement(82..111)
FT      /tag= c
FT      /product="ELVISLIVES protein"
FT      complement(119..148)
FT      /tag= d
FT      /product="ELVISLIVES protein"
XX      MO200216565-A2.
XX      28-FEB-2002.
XX      22-AUG-2001; 2001WO-US026246.
XX      22-AUG-2000; 2000US-0226996P.
XX      (DUBO ) DU PONT DE NEMOURS & CO E. I.
XX      Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX      WPI; 2002-269353/31.
XX      P-PsDB; AAE20554.
XX      New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX      useful in creating transgenic plants having altered levels of mono-, poly
XX      - and unsaturated fatty acids and in increasing the unsaturation levels
XX      in cellular lipids.
XX      Example 9; Page 43; 77pp; English.
XX      The present invention relates to diverged delta-9 fatty acid desaturase
XX      proteins and polynucleotides encoding such proteins. The nucleic acid
XX      sequences may be used to increase the level of unsaturation in cellular
XX      lipids, including oil, in tissues when the enzyme is absent or rate-
XX      limiting, to isolate cDNAs and genes encoding homologous proteins from
XX      the same or other plant species and to create transgenic plants in which
XX      the polypeptides are present at higher or lower levels than normal or in
XX      cell types or developmental stages in which they are not normally found,
XX      thus altering the level of mono-, poly- and unsaturated fatty acids in
XX      those cells. They are useful as probes for genetic and physical gene
XX      mapping and as markers, e.g. restriction fragment length polymorphism
XX      (RFLP) markers. The peptides can be used to immunise animals to produce
XX      antibodies specific for the peptides and proteins. The present sequence
XX      is a ELVISLIVES complementary repeat region DNA found in plasmid pKS133
XX      CC suppression of Fed2 in soybean
XX      Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 154; DB 6; Length 154;
XX      Best Local Similarity 100.0%; Pred. No. 2,7e-28;
XX      Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 60
DB      154 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 95
OY      61 CATCGTCAGTCGGGCGCGCGGAGTCGACGATGAGGAGATGACCAAGCTCCGCGCGG 120
DB      94 CATCGTCAGTCGGGCGCGCGGAGTCGACGATGAGGAGATGACCAAGCTCCGCGCGG 35
OY      121 ACTGAGCATGAGGAGATGACCAAGCTCCGCGCGG 154
DB      34 ACTGAGCATGAGGAGATGACCAAGCTCCGCGCGG 1
XX      RESULT 5
XX      AD007968
XX      AD007968 standard; DNA; 154 BP.
XX      AD007968;
XX      23-SEP-2004 (first entry)
```

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XX      /product="ELVISLIVES protein"
XX      complement(82..111)
XX      /tag= c
XX      /product="ELVISLIVES protein"
XX      complement(119..148)
XX      /tag= d
XX      /product="ELVISLIVES protein"
XX      MO200216565-A2.
XX      28-FEB-2002.
XX      22-AUG-2001; 2001WO-US026246.
XX      22-AUG-2000; 2000US-0226996P.
XX      (DUBO ) DU PONT DE NEMOURS & CO E. I.
XX      Booth JR, Cahoon RE, Hiltz WD, Kinney AJ, Yadav NS;
XX      WPI; 2002-269353/31.
XX      P-PsDB; AAE20554.
XX      New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX      useful in creating transgenic plants having altered levels of mono-, poly
XX      - and unsaturated fatty acids and in increasing the unsaturation levels
XX      in cellular lipids.
XX      Example 9; Page 43; 77pp; English.
XX      The present invention relates to diverged delta-9 fatty acid desaturase
XX      proteins and polynucleotides encoding such proteins. The nucleic acid
XX      sequences may be used to increase the level of unsaturation in cellular
XX      lipids, including oil, in tissues when the enzyme is absent or rate-
XX      limiting, to isolate cDNAs and genes encoding homologous proteins from
XX      the same or other plant species and to create transgenic plants in which
XX      the polypeptides are present at higher or lower levels than normal or in
XX      cell types or developmental stages in which they are not normally found,
XX      thus altering the level of mono-, poly- and unsaturated fatty acids in
XX      those cells. They are useful as probes for genetic and physical gene
XX      mapping and as markers, e.g. restriction fragment length polymorphism
XX      (RFLP) markers. The peptides can be used to immunise animals to produce
XX      antibodies specific for the peptides and proteins. The present sequence
XX      is a ELVISLIVES complementary repeat region DNA found in plasmid pKS133
XX      CC suppression of Fed2 in soybean
XX      Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 154; DB 6; Length 154;
XX      Best Local Similarity 100.0%; Pred. No. 2,7e-28;
XX      Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 60
DB      154 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 95
OY      61 CATCGTCAGTCGGGCGCGCGGAGTCGACGATGAGGAGATGACCAAGCTCCGCGCGG 120
DB      94 CATCGTCAGTCGGGCGCGCGGAGTCGACGATGAGGAGATGACCAAGCTCCGCGCGG 35
OY      121 ACTGAGCATGAGGAGATGACCAAGCTCCGCGCGG 154
DB      34 ACTGAGCATGAGGAGATGACCAAGCTCCGCGCGG 1
XX      Seed specific gene silencing vector pKS151, stem loop region.
XX      pKS151, seed specific promoter; gene silencing; chalcone reductase;
XX      transgenic; liguiritigenin-derived isoflavone; isoflavonoid;
XX      food product; snack food product; baked good product; fried food product;
XX      health food product; infant formula; beverage; nutritional supplement;
XX      dairy product; pet food product; animal feed; ss.
XX      Synthetic.
XX      Key      Location/Qualifiers
XX      stem_loop      1..154
XX      /*tag= a
XX      US2004128714-A1.
XX      01-JUL-2004.
XX      11-DEC-2003; 2003US-00734947.
XX      13-DEC-2002; 2002US-0433433P.
XX      (MCGO/) MCGONIGHE B.
XX      MCGonigle B;
XX      WPI; 2004-533136/51.
XX      Decreasing ratio of liguiritigenin-derived isoflavones relative to total
XX      isoflavones in a plant comprises transforming plant cell with nucleic
XX      acid sequence showing homology to sequence encoding chalcone reductase
XX      (deoxychalcone synthase).
XX      Example 7; SEQ ID NO 7; 25pp; English.
XX      The invention relates to decreasing the ratio of liguiritigenin-derived
XX      isoflavones relative to the total isoflavones in an isoflavonoid-
XX      producing plant comprising transforming a plant cell with a recombinant
XX      construct comprising a promoter operably linked to a nucleic acid
XX      sequence of at least 200 nucleotides having at least 75% sequence
XX      identity to AD007965 (a soybean chalcone reductase cDNA). Also included
XX      are an isoflavonoid-producing plant made by the method above, seeds or
XX      plant parts of the plant, an isoflavonoid-containing protein product
XX      having a reduced ratio of liguiritigenin-derived isoflavones relative to
XX      the total isoflavone levels obtained from the seeds or plant parts, a
XX      food (or a nutritional supplement, a food bar, or a beverage) which has
XX      incorporated the isoflavonoid-containing product, and a method of
XX      producing an isoflavonoid-containing product having a reduced ratio of
XX      liguiritigenin-derived isoflavones relative to the total isoflavone
XX      levels. The recombinant construct comprises a stem-loop structure. The
XX      nucleic acid sequence forms a loop in the stem-loop structure and the
XX      stem comprises a sequence of AD007968). The promoter is a seed-specific
XX      promoter. The method is useful for decreasing the ratio of liguiritigenin-
XX      derived isoflavones relative to the total isoflavones in an isoflavone-
XX      producing plant. The methods and recombinant construct are useful in
XX      producing an isoflavonoid-containing product which is incorporated in
XX      cereal food product, snack food product, baked good product, fried food
XX      product, health food product, infant formula, beverage, nutritional
XX      supplement, dairy product, pet food product, or animal feed. The present
XX      sequence is the single stranded version of the stem loop region from
XX      plasmid pKS151.
XX      Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX      Query Match      100.0%; Score 154; DB 12; Length 154;
XX      Best Local Similarity 100.0%; Pred. No. 2,7e-28;
XX      Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 60
DB      1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGGCGCGGAGCTGTCATCTGCT 60
```

CC	cereal food product, snack food product, baked good product, fried food
CC	product, health food product, infant formula, beverage, nutritional
CC	supplement, dairy product, pet food product, or animal feed. The present
CC	sequence is the single stranded version of the stem loop region from
CC	plasmid pKS151.
XX	
SQ	Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 154; DB 12; Length 154;
Best Local Similarity	100.0%; Pred. No. 2.7e-28;
Matches 154; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1 CGGCGGAGCTGGTCATCTGCCTCATGTGAGTCCGCGGCCGAGCTGTCATCTGCT 60
DB	154 CGGCGGAGCTGGTCATCTGCCTCATGTGAGTCCGCGGCCGAGCTGTCATCTGCT 95
OY	61 CATCGTGAGTCGGCGCGCCGCACTGACGATGAGGAGATGACCAGCTCCGCGCCG 120
DB	94 CATCGTGAGTCGGCGCGCCGCACTGACGATGAGGAGATGACCAGCTCCGCGCCG 35
OY	121 ACTGACGATGAGCGAGATGACCAAGCTCCGCGC 154
DB	34 ACTGACGATGAGCGAGATGACCAAGCTCCGCGC 1
RESULT 7	
ID	ABK10711
ID	ABK10711 standard; DNA; 81 BP.
XX	
AC	ABK10711;
XX	
DT	05-JUN-2002 (first entry)
XX	
DE	Artificial DNA sequence #3.
XX	
KX	Plastidic phosphoglucomutase; transgenic; plant; gene; ds.
XX	
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	CDS 7..36
FT	/tag= a
FT	/product= "ELVISLIVES peptide"
FT	/partial
FT	/note= "No start or stop codon shown"
FT	44..73
FT	/tag= b
FT	/product= "ELVISLIVES peptide"
FT	/partial
FT	/note= "No start or stop codon shown"
XX	
PN	EPI174510-A2.
XX	
PB	23-JAN-2002.
XX	
PF	17-JUL-2001; 2001EP-00306143.
XX	
PR	17-JUL-2000; 2000US-0218712P.
XX	
PA	(DUPLO) DU PONT DE NEMOURS & CO E I.
XX	
P1	Allen SM, Butler KH, Carlson TV, Ilag LT;
XX	
DR	WPI: 2002-156692/21.
XX	
DR	P-PSTDB; MAU77109.
XX	
PT	Novel isolated polypeptides having phosphoglucomutase activity and
XX	
PT	polynucleotides encoding the polypeptides, useful for producing
XX	
PT	transgenic plants with altered plastidic phosphoglucomutase protein
XX	
XX	levels.
XX	
PS	Example 9; Page 19; 27pp; English.
XX	

CC The invention relates to plastidic phosphoglucumutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucumutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucumutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucumutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucumutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

CC Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;

CC Query Match 52.6%; Score 81; DB 6; Length 81;

CC Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 CGGCGGAGCTGTCATCTGCTCATCTGTCGAGTGGCGGCGGAGCTGTCATCTGCT 60

CC 1 CGGCGGAGCTGTCATCTGCTCATCTGTCGAGTGGCGGCGGAGCTGTCATCTGCT 60

CC 61 CATGCTCGAGTCGGCGGCGCG 81

CC 61 CATGCTCGAGTCGGCGGCGCG 81

CC RESULT 8
CC ABK10711/C
CC ID ABK10711 standard; DNA; 81 BP.

CC XX ABK10711;

CC XX 05-JUN-2002 (first entry)

CC XX Artificial DNA sequence #3.

CC XX Plastidic phosphoglucumutase; transgenic; plant; gene; ds.

CC XX Synthetic.

CC XX Key Location/Qualifiers

CC XX CDS 7..36
CC XX /*tag= a
CC XX /product= "ELVISLIVES peptide"
CC XX /partial
CC XX /note= "No start or stop codon shown"

CC XX CDS 44..73
CC XX /*tag= b
CC XX /product= "ELVISLIVES peptide"
CC XX /partial
CC XX /note= "No start or stop codon shown"

CC XX EP1174510-A2.

CC XX 23-JAN-2002.

CC XX 17-JUL-2001; 2001EP-00306143.

CC XX 17-JUL-2000; 2000US-0218712P.

CC XX (DUPO) DU PONT DE NEMOURS & CO E I.

PI Allen SM, Butler KH, Carlson TV, Ilag LL;
XX WPI; 2002-156692/21.
DR P-PSDB; AA077109.

CC Novel isolated polypeptides having phosphoglucumutase activity and
CC polynucleotides encoding the polypeptides, useful for producing
CC transgenic plants with altered plastidic phosphoglucumutase protein
CC levels.

CC Example 9, Page 19; 27pp; English.

CC The invention relates to plastidic phosphoglucumutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucumutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucumutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucumutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucumutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

CC Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;

CC Query Match 52.6%; Score 81; DB 6; Length 81;

CC Best Local Similarity 100.0%; Pred. No. 1.3e-10; Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 74 GCGGCGGCGGAGCTGTCGAGTGGAGGAGTGCAGTCTCGGCGGCGGAGTGCAGTGCAG 133

CC 81 GCGGCGGCGGAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAGTGCAG 22

CC 134 CGAGATGACCGAGCTCCGCGCG 154

CC 21 CGAGATGACCGAGCTCCGCGCG 1

CC RESULT 9
CC AAD29230
CC ID AAD29230 standard; DNA; 80 BP.

CC XX AAD29230;

CC XX 07-MAY-2002 (first entry)

CC XX Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.

CC XX Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
CC ds.

CC XX Unidentified.

CC XX Key Location/Qualifiers

CC XX CDS 7..36
CC XX /*tag= a
CC XX /product= "ELVISLIVES protein"
CC XX /partial
CC XX /tag= b
CC XX /product= "ELVISLIVES protein"

CC XX WO200200904-A2.


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XX 03-JAN-2002.
PD 22-JUN-2001; 2001WO-US019962.
XX 23-JUN-2000; 2000US-0213961P.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI Nichols SE;
XX WPI; 2002-139927/18.
DR P-PSDB; AAE18333.
XX
XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
XX Claim 45; Page 37; 77pp; English.
XX
XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
XX Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
SQ
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
DB 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 60
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 61 GAGATGACCAAGCTCCGGCCG 80
RESULT 10
AAD29230/C
ID AAD29230 standard; DNA; 80 BP.
XX
XX AAD29230;
AC
XX 07-MAY-2002 (first entry)
DT
XX Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
DE
XX Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
KM ds.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH 7..36
FT /product= a
FT /product= "ELVISLIVES protein"
FT CDS
FT CDS
FT CDS
```

```
PT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX WO200200904-A2.
XX
XX 03-JAN-2002.
PD
XX 22-JUN-2001; 2001WO-US019962.
XX 23-JUN-2000; 2000US-0213961P.
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI Nichols SE;
XX WPI; 2002-139927/18.
DR P-PSDB; AAE18333.
XX
XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
XX Claim 45; Page 37; 77pp; English.
XX
XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
XX Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
SQ
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 97
DB 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCCGCCGACTCGACGATGAGC 21
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 20 GAGATGACCAAGCTCCGGCCG 1
RESULT 11
AAD32907
ID AAD32907 standard; DNA; 80 BP.
XX
XX AAD32907;
AC
XX 01-JUN-2002 (first entry)
DT
XX Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
DE
XX Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
KM transgenic plant; gene mapping; immunisation; plasmid pKS124;
KM plasmid pKS106; gene; ds.
XX
XX Unidentified.
XX
```


DT 05-JUN-2002 (first entry)
XX Artificial DNA sequence #4.
DE
XX Plasticidic phosphoglucomutase; transgenic; plant; gene; ss.
KM
XX Synthetic.
OS
XX EP1174510-A2.
PN
XX 23-JAN-2002.
PD
XX 17-JUL-2001; 2001EP-00306143.
PF
XX 17-JUL-2000; 2000US-0218712P.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA Allen SM, Butler KH, Carlson TJ, Ilag LJ;
PI WPI; 2002-156692/21.
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plasticidic phosphoglucomutase protein
PT levels.
XX
XX Example 9; Page 19; 27pp; English.
PS
XX The invention relates to plasticidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plasticidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plasticidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plasticidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plasticidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTGCAGCATGAGC 97
DB 7 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTGCAGCATGAGC 66
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 67 GAGATGACCAAGCTCCGGCCG 86

RESULT 14
ABK10712/c
ID ABK10712 standard; DNA; 92 BP.
XX
XX ABK10712;
AC
XX 05-JUN-2002 (first entry)
DT

XX
XX Artificial DNA sequence #4.
DE
XX Plasticidic phosphoglucomutase; transgenic; plant; gene; ss.
KM
XX Synthetic.
OS
XX EP1174510-A2.
PN
XX 23-JAN-2002.
PD
XX 17-JUL-2001; 2001EP-00306143.
PF
XX 17-JUL-2000; 2000US-0218712P.
PR
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA Allen SM, Butler KH, Carlson TJ, Ilag LJ;
PI WPI; 2002-156692/21.
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plasticidic phosphoglucomutase protein
PT levels.
XX
XX Example 9; Page 19; 27pp; English.
PS
XX The invention relates to plasticidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plasticidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plasticidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plasticidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plasticidic phosphoglucomutase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTGCAGCATGAGC 97
DB 86 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTCGGCGCGCCGCACTGCAGCATGAGC 27
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 26 GAGATGACCAAGCTCCGGCCG 7

RESULT 15
AAD29232
ID AAD29232 standard; DNA; 92 BP.
XX
XX AAD29232;
AC
XX 07-MAY-2002 (first entry)
DT
XX

DE ELVISLIVES complementary region DNA amplifying PCR primer #1.
XX
XX Recombinant construct; gene expression; PCR primer; ss.
XX
XX Unidentified.
OS
XX WO200200904-A2.
XX
XX 03-JAN-2002.
XX
XX 22-JUN-2001; 2001WO-US019962.
XX
XX 23-JUN-2000; 2000US-0213961P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Glasman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
XX Nichols SE;
XX
XX WPI; 2002-139927/18.
XX
XX
XX New recombinant construct having a promoter operably linked to a DNA
XX sequence which when expressed produces an RNA having homology to a target
XX mRNA and its reverse complement unrelated to endogenous DNA, for reducing
XX gene expression.
XX
XX Example 7; Page 37; 77pp; English.
XX
XX The present invention relates to a new recombinant construct. The
XX construct comprises a promoter operably linked to a DNA sequence which
XX when expressed by a host produces an RNA having homology to at least one
XX target mRNA expressed by the host and complementary RNA regions. The
XX recombinant construct is useful for reducing the expression of a target
XX mRNA or any similar endogenous mRNA. The RNAs expressed from the
XX recombinant constructs are also used in reducing expression of a target
XX mRNA or any similar endogenous mRNA. The sequences and their reverse
XX complements can be used to reduce the expression of any endogenous
XX genomic sequence that shares substantial similarity to nucleic acid
XX fragment which is in proximity to the DNA or RNA sequence derived from
XX it. The present sequence is a PCR primer used for amplifying ELVISLIVES
XX complementary region DNA used in the exemplification of the invention
XX
XX Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
XX
XX
XX Query Match 51.9%; Score 80; DB 6; Length 92;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 38 CGGCCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCGACTCGACGATGAGC 97
XX |||||||
XX Db 7 CGGCCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCGACTCGACGATGAGC 66
XX |||||||
XX QY 98 GAGATGACCACTCCGGCCG 117
XX |||||||
XX Db 67 GAGATGACCACTCCGGCCG 86
XX
XX
XX RESULT 16
XX AAD29232/C
XX ID AAD29232 standard; DNA; 92 BP.
XX AC AAD29232;
XX
XX 07-MAY-2002 (first entry)
XX
XX ELVISLIVES complementary region DNA amplifying PCR primer #1.
XX
XX Recombinant construct; gene expression; PCR primer; ss.
XX
XX Unidentified.
XX
XX WO200200904-A2.
XX
XX PN

XX
XX 03-JAN-2002.
XX
XX 22-JUN-2001; 2001WO-US019962.
XX
XX 23-JUN-2000; 2000US-0213961P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Glasman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
XX Nichols SE;
XX
XX WPI; 2002-139927/18.
XX
XX
XX New recombinant construct having a promoter operably linked to a DNA
XX sequence which when expressed produces an RNA having homology to a target
XX mRNA and its reverse complement unrelated to endogenous DNA, for reducing
XX gene expression.
XX
XX Example 7; Page 37; 77pp; English.
XX
XX The present invention relates to a new recombinant construct. The
XX construct comprises a promoter operably linked to a DNA sequence which
XX when expressed by a host produces an RNA having homology to at least one
XX target mRNA expressed by the host and complementary RNA regions. The
XX recombinant construct is useful for reducing the expression of a target
XX mRNA or any similar endogenous mRNA. The RNAs expressed from the
XX recombinant constructs are also used in reducing expression of a target
XX mRNA or any similar endogenous mRNA. The sequences and their reverse
XX complements can be used to reduce the expression of any endogenous
XX genomic sequence that shares substantial similarity to nucleic acid
XX fragment which is in proximity to the DNA or RNA sequence derived from
XX it. The present sequence is a PCR primer used for amplifying ELVISLIVES
XX complementary region DNA used in the exemplification of the invention
XX
XX Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
XX
XX
XX Query Match 51.9%; Score 80; DB 6; Length 92;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-10;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 38 CGGCCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCGACTCGACGATGAGC 97
XX |||||||
XX Db 86 CGGCCGAGCTGTCATCTCGTCATCGTCGAGTCGGCGCGCGACTCGACGATGAGC 27
XX |||||||
XX QY 98 GAGATGACCACTCCGGCCG 117
XX |||||||
XX Db 26 GAGATGACCACTCCGGCCG 7
XX
XX
XX RESULT 17
XX ABK10710
XX ID ABK10710 standard; DNA; 44 BP.
XX AC ABK10710;
XX
XX 05-JUN-2002 (first entry)
XX
XX Artificial DNA sequence #2.
XX
XX Plasmidic phosphoglucomutase; transgenic; plant; gene; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 7.36
XX FT /*tag= a
XX FT /product= "ELVISLIVES peptide"
XX FT /partial
XX FT /note= "No start or stop codon shown"
XX
XX PN BP1174510-A2.

XX	PD	23-JAN-2002.
XX	PF	17-JUL-2001; 2001EP-00306143.
XX	PR	17-JUL-2000; 2000US-0218712P.
PA	(DUPO) DU PONT DE NEMOURS & CO E I.	
PA	Allan SM, Butler KH, Carlson TJ, Ilag LL;	
XX	WPI; 2002-156692/21.	
DR	P-PSDB, AAV77109.	
XX		
PS	Example 9; Page 19; 27pp; English.	
XX	The invention relates to plasmidic phosphoglucomutase polypeptides and	
CC	their related nucleic acids. The sequences are useful for producing a	
CC	transgenic plant, by transforming a plant cell with a polynucleotide of	
CC	the invention and regenerating a plant from the transformed plant cell.	
CC	polynucleotide fragments are useful for suppressing the level of	
CC	expression of a gene encoding a polypeptide having plasmidic	
CC	phosphoglucomutase activity. An isolated polynucleotide that affects the	
CC	level of expression of a plasmidic phosphoglucomutase polypeptide in a	
CC	plant cell can be identified by introducing a DNA fragment comprising at	
CC	least 541 nucleotides, measuring the level of the polypeptide in the	
CC	plant cell containing the polynucleotide, and comparing the level of the	
CC	polypeptide in the plant cell containing the isolated polynucleotide with	
CC	the level of the polypeptide in a plant cell that does not contain the	
CC	isolated polynucleotide. A method for altering the level of expression of	
CC	a plasmidic phosphoglucomutase protein in a host cell comprises	
CC	transforming a host cell with a chimeric gene and growing the transformed	
CC	cell under conditions that are suitable for expression of the chimeric	
CC	gene, where the expression of the gene results in production of altered	
CC	levels of plasmidic phosphoglucomutase. This sequence represents an	
CC	artificial DNA used for plasmid construction, in the methods of the	
XX	invention	
SQ	Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;	
Query Match	28.6%; Score 44; DB 6; Length 44;	
Best Local Similarity	100.0%; Pred. No. 0.12;	
Matches 44; Conservative	0; Mismatches 0; Indels 0; Gaps 0	
QY	38 CGGCCGAGCTGGTCATCTCGCTCATCGTGCAGTGCGGCCGC 81	
Dd	1 CGGCCGAGCTGGTCATCTCGCTCATCGTGCAGTGCGGCCGC 44	
RESULT 18		
ABK10710/c		
ID	ABK10710 standard; DNA; 44 BP.	
AC	ABK10710;	
DT	05-JUN-2002 (first entry)	
DE	Artificial DNA sequence #2.	
KM	Plasmidic phosphoglucomutase; transgenic; plant; gene; ds.	
OS	Synthetic.	
Key	Location/Qualifiers	
CDS	7..36	
/tag=	a	
/product=	"ELVISLIVES peptide"	
/partial		

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FT      /note= "No start or stop codon shown"
FM      EPI174510-A2.
FX      23-JAN-2002.
XX
XX      17-JUL-2001; 2001EP-00306143.
XX      17-JUL-2000; 2000US-0218712P.
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Allen SM, Butler KH, Carlson TJ, Ilag LL,
PI      WPI; 2002-156692/21.
XX      P-PSDB; AAU77109.
DR
XX      Novel isolated polypeptides having phosphoglucomutase activity and
PT      polynucleotides encoding the polypeptides, useful for producing
PT      transgenic plants with altered plastidic phosphoglucomutase protein
PT      levels.
XX
XX      Example 9; Page 19; 27pp; English.
XX
XX      The invention relates to plastidic phosphoglucomutase polypeptides and
CC      their related nucleic acids. The sequences are useful for producing a
CC      transgenic plant. By transforming a plant cell with a polynucleotide of
CC      the invention and regenerating a plant from the transformed plant cell.
CC      Polynucleotide fragments are useful for suppressing the level of
CC      expression of a gene encoding a polypeptide having plastidic
CC      phosphoglucomutase activity. An isolated polynucleotide that affects the
CC      level of expression of a plastidic phosphoglucomutase polypeptide in a
CC      plant cell can be identified by introducing a DNA fragment comprising at
CC      least 541 nucleotides, measuring the level of the polypeptide in the
CC      plant cell containing the polynucleotide, and comparing the level of the
CC      polypeptide in the plant cell containing the isolated polynucleotide with
CC      the level of the polypeptide in a plant cell that does not contain the
CC      isolated polynucleotide. A method for altering the level of expression of
CC      a plastidic phosphoglucomutase protein in a host cell comprises
CC      transforming a host cell with a chimeric gene and growing the transformed
CC      cell under conditions that are suitable for expression of the chimeric
CC      gene, where the expression of the gene results in production of altered
CC      levels of plastidic phosphoglucomutase. This sequence represents an
CC      artificial DNA used for plasmid construction, in the methods of the
CC      invention
XX
XX      Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      28.6%; Score 44; DB 6; Length 44;
XX      Best Local Similarity 100.0%; Pred. No. 0.12;
XX      Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
OY      74 GCGGCGCGCGACCTGCAGATGAGAGATGACCACTCCGGCGG 117
DB      44 GCGGCGCGCGACCTGCAGATGAGAGATGACCACTCCGGCGG 1
XX
XX      RESULT 19
AAC89216
ID      AAC89216 standard; DNA; 194 BP.
XX
XX      AAC89216;
XX
XX      07-MAR-2001 (first entry)
XX
XX      Human brain T calcium channel alpha 1G subunit gene exon 16.
DE
XX      Ion channel; human; brain T calcium channel; alpha 1G subunit;
KW      alpha 1I subunit; epilepsy; drug screening; ds.
XX
XX      Homo sapiens.
OS
XX      MO200070044-A2.
XX

```

XX 23-NOV-2000.
PD 08-MAY-2000; 2000WO-US012383.
XX
PF 13-MAY-1999; 99US-0134063P.
XX PR 04-JUN-1999; 99US-0137547P.
XX
PA (UJJO) UNIV JOHNS HOPKINS.
XX
PI Miltman S, Agnew WS;
XX
DR WPI; 2001-031928/04.
DR P-PSDB; AAB50116.
XX
PT Splice variants of the human brain T calcium channel alpha 1G and alpha
PT 1I subunits and genes encoding the subunits, useful as targets for
PT antiepileptic drugs or for testing compounds or compositions useful in
PT treating epilepsy.
XX
PS Claim 5; Page 19; 89pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha
CC 1G subunit gene (designated CACNA1G) consists of 38 exons, and
CC alternative processing leads to the production of 64 different proteins.
CC The alpha 1I subunit (designated CACNA1I) consists of 37 exons, and 8
CC proteins are produced due to alternative processing. The sequences
CC provided by the invention are useful for screening drugs for use in the
CC treatment of epilepsy.
XX
SQ Sequence 194 BP; 33 A; 72 C; 67 G; 22 T; 0 U; 0 Other;
XX
Query Match 19.1%; Score 29.4; DB 4; Length 194;
Best Local Similarity 58.6%; Pred. No. 4.2e+02;
Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 30 CGAGTCGCGCGCGAGCTGTCATCTGCTCATGTCGAGTCGCGCGCGCGACTCGA 89
DB 22 CGAGCTCGCGAAGAGCTGCTGCGCGCTCTCATCTCAACAGCGCGCCACACCATGT 81
QY 90 CGATGAGCGAGATGACCAAGCTCCGCGC 116
DB 82 CGCTGCCCAAGACACCGACGCGGCGC 108
XX
RESULT 20
AAC89216/c
ID AAC89216 standard; DNA; 194 BP.
XX
AC AAC89216;
XX
DT 07-MAR-2001 (first entry)
XX
DE Human brain T calcium channel alpha 1G subunit gene exon 16.
XX
KW Ion channel; human; brain T calcium channel; alpha 1G subunit;
KW alpha 1I subunit; epilepsy; drug screening; ds.
XX
OS Homo sapiens.
XX
PN WO200070044-A2.
XX
PD 23-NOV-2000.
XX
PF 08-MAY-2000; 2000WO-US012383.
XX
PR 13-MAY-1999; 99US-0134063P.
XX PR 04-JUN-1999; 99US-0137547P.
XX
PA (UJJO) UNIV JOHNS HOPKINS.
XX
PI Miltman S, Agnew WS;

XX
DR WPI; 2001-031928/04.
DR P-PSDB; AAB50116.
XX
PT Splice variants of the human brain T calcium channel alpha 1G and alpha
PT 1I subunits and genes encoding the subunits, useful as targets for
PT antiepileptic drugs or for testing compounds or compositions useful in
PT treating epilepsy.
XX
PS Claim 5; Page 19; 89pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human brain T calcium channel alpha 1G and alpha 1I subunits. The alpha
CC 1G subunit gene (designated CACNA1G) consists of 38 exons, and
CC alternative processing leads to the production of 64 different proteins.
CC The alpha 1I subunit (designated CACNA1I) consists of 37 exons, and 8
CC proteins are produced due to alternative processing. The sequences
CC provided by the invention are useful for screening drugs for use in the
CC treatment of epilepsy.
XX
SQ Sequence 194 BP; 33 A; 72 C; 67 G; 22 T; 0 U; 0 Other;
XX
Query Match 19.1%; Score 29.4; DB 4; Length 194;
Best Local Similarity 58.6%; Pred. No. 4.2e+02;
Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 39 GCGCGAGCTGTCATCTGCTCATGTCGAGTCGCGCGCGCGACTCGAGGCG 98
DB 108 GCGCGCTGCTGCTCTTGTGGCGAGCATGGGTGTGGCGCGCTGTGATGATGAGG 49
QY 99 AGATGACCAAGCTCCGCGCGCGACTCG 125
DB 48 GCGGACAGAGCTCTTCCGACGCTCCG 22
XX
RESULT 21
ABX88193
ID ABX88193 standard; cDNA; 197 BP.
XX
AC ABX88193;
XX
DT 24-APR-2003 (first entry)
XX
DE Corn ear-derived polynucleotide (cpd) #6653.
XX
KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;
KW structural gene; functional gene; regulatory gene;
KW corn ear-specific profile; gene transcription; gene expression;
KW hybrid plant; desirable trait expression; plant breeding program;
KW inheritance; desired characteristic; growth; development;
KW disease resistance; environmental adaptability; quality; yield;
KW multigene trait; plant; gene; ss.
XX
OS Zea mays.
XX
PN US6476212-B1.
XX
PD 05-NOV-2002.
XX
PF 14-MAY-1999; 99US-00313294.
XX PR 26-MAY-1998; 98US-0086722P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lalajudi RV, Ico IX, Sherman BK;
XX
DR WPI; 2003-208840/20.
XX
PT Novel purified corn-ear derived polynucleotide useful as hybridization
PT probe for detecting polynucleotide in sample, and for identifying,
PT evaluating, and altering desired characteristics associated with growth,
PT development.

XX	
PS	Example; SEQ ID NO 6653; 390pp; English

The present invention relates to the isolation of corn ear-derived polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022 and SATMON023. Some of the cdfs uniquely identify structural, functional, and regulatory genes of corn ear. The polynucleotides sequences are useful for detecting cdfs in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in inbred or hybrid plants, and for screening several molecules for specific binding to the polynucleotide. The cdfs are useful to identify, isolate, or extend identical or related corn-ear nucleic acid sequences from DNA libraries, and in nucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding programs. Preferably, the cdfs are used to identify, evaluate, alter, or follow the inheritance of desired characteristics associated with growth and development, disease resistance, environmental adaptability, quality, and yield of corn. The cdfs are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cdfs are useful for producing purified corn-ear polypeptides by recombinant techniques. They are also useful in diagnostic assays to detect or confirm conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn ear-derived polynucleotides (cdfs) of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site at www.uspto.gov/patidentry.html

Sequence 197 BP; 42 A; 55 C; 68 G; 30 T; 0 U; 2 Other;

Query Match	18.2%	Score 28	DB 10	Length 197
Best Local Similarity	51.2%	Pred. No. 9.1e+02		
Matches 64, Conservative		0	Mismatches 61	Indels 0
			Gaps	0

Qy	Db	Qy	Db
28	63	88	123
GTGAGATCGGGCGGCGAGTGGTATCTGGCTATACGTCAAGTGGGGCGGCGA	GGGGCGGATGTCGCCCGGACTGTCTCTGGCCCGACAGCTGTACNTCTCTCA	GACGATGAGCGAGATGACCAAGCTCGGGCTCGGCGACTCGACATGAGCGAGTACCA	AGTCAGAGCGACATGGTGGTCGGCGCGCGAGATGACCGAAGAGCGCGGAGGACGGA
87	122	147	182
CTC	CTC	GCT	GGA

Qy	148	CCGGC	152
Db	183	GCAGC	187

RESULT 22
ABX88193/c
ID ABX88193 standard; cDNA; 197 BP.

AC ABX88193;

DT 24-APR-2003 (first entry)

Corn ear-derived polynucleotide (cpd) #6653.

KM ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023
KM structural gene; functional gene; regulatory gene;
KM corn ear-specific profile; gene transcription; gene expression;
KM hybrid plant; desirable trait expression; plant breeding program;
KM inheritance; desirable characteristics; growth; development;
KM disease resistance; environmental adaptability; quality; yield;
KM multigene trait; plant; gene; ss.

OS Zea mays.

PN US6476212-B1.

PD 05-NOV-2002

PF 14-MAY-1999; 99US-00313294.

PR 26-MAY-1998; 98US-0086722P.

PA (INCY-) INCYTE GENOMICS INC.

PI Lalgudi RV, Ito LY, Sherman BK;

DR WPI; 2003-208840/20

Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with growth, development.

PS Example; SEQ ID NO 6653; 390pp; English.

CC The present invention relates to the isolation of corn ear-derived
CC polynucleotides (cdps) from the corn (zea mays) cDNA libraries SATM0022
CC and SATM0023. Some of the cpts uniquely identify structural, functional,
CC and regulatory genes of corn ear. The polynucleotide sequences are
CC useful for detecting cpts in a sample, for producing a corn ear-specific
CC profile of gene transcription, for detecting altered gene expression in
CC inbred or hybrid plants, and for screening several molecules for specific
CC binding to the polynucleotide. The cpts are useful to identify, isolate,
CC or extend identical or related corn-ear nucleic acid sequences from DNA
CC libraries, and in nucleic acid amplification or hybridization techniques
CC to follow the expression of desirable traits through plant breeding
CC programs. Preferably, the cpts are used to identify, evaluate, alter, or
CC follow the inheritance of desired characteristics associated with growth
CC and development, disease resistance, environmental adaptability, quality,
CC and yield of corn. The cpts are also useful as molecular markers for
CC studying inheritance and multigene traits in a plant breeding program.
CC The cpts are useful for producing purified corn-ear polypeptides by
CC recombinant techniques. They are also useful in diagnostic assays to
CC detect or confirm conditions or diseases associated with abnormal levels
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived
CC polynucleotides (cpts) of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the USPTO web site at
CC seqdata.uspto.gov/ps/psidDetail.html

Sequence 197 BP; 42 A; 55 C; 68 G; 30 T; 0 U; 2 Other;

Query Match	18.2%	Score 28	DB 10	Length 197
Best Local Similarity	51.2%	Pred. No.	9.1e+02	
Matches 64	Conservative 0	Mismatches 61	Indels 0	Gaps 0

[illegible]

QY 123 TCGAC 127
Db 67 GCGCC 63

RESULT 23
AAL44709
ID AAL44709 standard; DNA; 156 BP

AC AAL44709;

DT 03-MAY-2002 (first entry)

DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 9.

KM Human, glutamate receptor delta-1 subunit; epilepsy; brain damage;
KM neurodegenerative disorder; Huntington's disease; Parkinson's disease
KM Alzheimer's disease; schizophrenia; mood disorder; dementia;
KM neuropathological pain; pain; receptor; anticonvulsant; nootropic;

KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX Homo sapiens.
XX WO200206313-A2.
XX 24-JAN-2002.
XX 13-JUL-2001; 2001WO-EP008102.
XX 18-JUL-2000; 2000US-0218835P.
XX (FARB) BAYER AG.
XX Kossida S;
XX WPI; 2002-195800/25.
XX
XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX
XX Claim 19; Fig 9; 97pp; English.
XX
XX The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 156 BP; 41 A; 45 C; 44 G; 26 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 156;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 60 TCATCGTCGAGTCGGCGCGCGGCGGAGCTGACGATGAGCGAGATACCACTCCGCGCGCC 119
DB 8 TCTTCGAGGAGACGCGCGGCGGAGCGACGAGGAGTTCGATGCGGATCCGACCTGA 67
QY 120 GACTCGACGATGA 132
DB 68 GCCTCAACGATGA 80
RESULT 24
AAL44709/c
ID AAL44709 standard; DNA; 156 BP.
AC AAL44709;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 9.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathologic pain; pain; receptor; anticonvulsant; nootropic;
KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200206313-A2.
XX 24-JAN-2002.
XX

PF 13-JUL-2001; 2001WO-EP008102.
XX
PR 18-JUL-2000; 2000US-0218835P.
XX
XX (FARB) BAYER AG.
XX
XX Kossida S;
XX WPI; 2002-195800/25.
XX
XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostate hyperplasia and urinary
PT incontinence.
XX
XX Claim 19; Fig 9; 97pp; English.
XX
XX The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 156 BP; 41 A; 45 C; 44 G; 26 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 156;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 23 TCATCGTCGAGTCGGCGCGCGGCGGAGCTGATTCGTCATCGATCGCGCGCGCC 82
DB 80 TCTTCGAGGAGTCGAGTCGATGATCCGCACTGAAACCTGTCGCTTGGCGCG 21
QY 83 GACTCGACGATGA 95
DB 20 TTCTCCGCAAGA 8
RESULT 25
AAL44706
ID AAL44706 standard; DNA; 190 BP.
AC AAL44706;
XX
DT 03-MAY-2002 (first entry)
XX
DE Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 2.
XX
KW Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KW Alzheimer's disease; schizophrenia; mood disorder; dementia;
KW neuropathologic pain; pain; receptor; anticonvulsant; nootropic;
KW neuroprotective; vasotropic; analgesic; neuroleptic; cytostatic;
KW uropathic; antiparkinsonian; vulnerary; gene; ds.
XX
OS Homo sapiens.
XX
XX WO200206313-A2.
XX 24-JAN-2002.
XX 13-JUL-2001; 2001WO-EP008102.
XX 18-JUL-2000; 2000US-0218835P.
XX (FARB) BAYER AG.
XX Kossida S;
XX WPI; 2002-195800/25.
XX

XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostatic hyperplasia and urinary
PT incontinence.
XX
XX
PS Disclosure; Fig 2; 97pp; English.
XX
XX The present invention provides a human glutamate receptor delta-1 subunit
CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 190 BP; 45 A; 57 C; 53 G; 35 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 190;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 60 TCATCGTCGAGTCGCGCGCGCGCGACTCGACGATGAGCGAGATGACCGCTCCGCGCGC 119
DB 20 TCTTCGAGGAGAACGCGCGCCAGAGACGACGAGGTCTTCATCTTGCGGTATCCGACCTGA 79
QY 120 GACTCGACGATGA 132
DB 80 GCCTCAACGATGA 92
RESULT 26
AAL44706/c
ID AAL44706 standard; DNA; 190 BP.
XX
XX AAL44706;
AC
XX
DT 03-MAY-2002 (first entry)
XX
XX Human glutamate receptor delta-1 subunit coding sequence SEQ ID NO: 2.
XX
XX Human; glutamate receptor delta-1 subunit; epilepsy; brain damage;
KM neurodegenerative disorder; Huntington's disease; Parkinson's disease;
KM Alzheimer's disease; schizophrenia; mood disorder; dementia;
KM neuropathologic pain; pain; receptor; anticonvulsant; nootropic;
KM neuroprotective; vasotropic; analgesic; neuroleptic; cycostatic;
KM utropathic; antiparkinsonian; vulnerary; gene; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200206313-A2.
PN
XX
XX 24-JAN-2002.
PD
XX
XX 13-JUL-2001; 2001WO-EP008102.
PF
XX
XX 18-JUL-2000; 2000US-0218935P.
PR
XX
XX (FARB) BAYER AG.
PA
XX
XX Kossida S;
PI
XX
XX WPI; 2002-195800/25.
DR
XX
XX Novel human glutamate receptor delta-1 subunit protein which can be
PT regulated for treating epilepsy, schizophrenia, neurodegenerative
PT diseases, ischemia, pain, benign prostatic hyperplasia and urinary
PT incontinence.
XX
XX Disclosure; Fig 2; 97pp; English.
PS
XX The present invention provides a human glutamate receptor delta-1 subunit

CC polypeptide. This can be used to screen for agents which modulate the
CC activity of glutamate receptor delta-1 subunit polypeptide, which may
CC then be used in the treatment of diseases such as epilepsy, brain damage,
CC neurodegenerative disorders such as Alzheimer's disease, Huntington's
CC disease and Parkinson's disease, schizophrenia, mood disorders, pain,
CC neuropathologic pain and dementias. The present sequence is a fragment of
CC the human glutamate receptor delta-1 subunit coding sequence
XX
SQ Sequence 190 BP; 45 A; 57 C; 53 G; 35 T; 0 U; 0 Other;
Query Match 17.3%; Score 26.6; DB 6; Length 190;
Best Local Similarity 60.3%; Pred. No. 2e+03;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 23 TCATCGTCGAGTCGCGCGCGCGCGACTGTCATCTCGTCGACGTCGCGCGCGC 82
DB 92 TCATCGTTGAGGCTCAGGTGCGATACCGCAACGACACCCGTCTCTTGCGCGC 33
QY 83 GACTCGACGATGA 95
DB 32 TCTTCCTCGAAGA 20
RESULT 27
AAC09904
ID AAC09904 standard; cDNA; 195 BP.
XX
XX AAC09904;
AC
XX
DT 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 13979.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KM gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
OS
XX
XX EPI033401-A2.
PN
XX
XX 06-SEP-2000.
PD
XX
XX 21-FEB-2000; 2000EP-00200610.
PF
XX
XX 26-FEB-1999; 99US-0122487P.
PR
XX
XX (GSET) GENSET.
PA
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
PI
XX
XX WPI; 2000-500381/45.
DR
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
PT
XX
XX Claim 1; SEQ ID NO 13979; 71pp + Sequence Listing; English.
PS
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
CC identified within the present sequence. The 5' ESTs were prepared from
CC total human RNAs or polyA- RNAs derived from 30 different tissues. EST
CC sequences usually correspond mainly to the 3' untranslated region (UTR)
CC of the mRNA because they are often obtained from oligo-dT primed cDNA
CC libraries. Such ESTs are not well suited for isolating cDNA sequences
CC derived from the 5' ends of mRNAs and even in those cases where longer
CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
CC ESTs are derived from mRNAs with intact 5' ends and can therefore be used
CC to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC They are used to obtain upstream regulatory sequences and to design
CC expression and secretion vectors
XX

Sequence 195 BP; 23 A; 79 C; 58 G; 32 T; 0 U; 3 Other;

Query Match 17.3%; Score 26.6; DB 3; Length 195;

Best Local Similarity 56.2%; Pred. No. 2e+03; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 37 GCGGCGGAGCTGTCATCTCGCTCATCTGTCGAGTGGCGGCGGAGTCCGACGATGAG 96
DB 46 GCTGCGGCGGCGGTGTCTGCGTTCGCGGAGATTTCTCTGCTCGGCTCGGCTCCTAGT 105
QY 97 CGAGATGACCACTCCGCGCCGCGGACTCG 125
DB 106 CTACGTCCCGAGCTCCAGCCGCGGCTCG 134

RESULT 28

AAC09904/C

ID AAC09904 standard; cDNA; 195 BP.

AAC09904;

06-OCT-2000 (first entry)

Human secreted protein 5' EST, SEQ ID NO: 13979.

Human, 5' EST, expressed sequence tag; secreted protein; cDNA isolation;

gene therapy; chromosome mapping; ss.

Homo sapiens.

EP1033401-A2.

06-SEP-2000.

21-FEB-2000; 2000EP-00200610.

26-FEB-1999; 99US-0122487P.

(GENSET)

Dumas Milne Edwards J, Duclert A, Giordano J;

WPI; 2000-500381/45.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for
obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
diagnostic, forensic, gene therapy and chromosome mapping procedures.

Claim 1; SEQ ID NO 13979; 71pp + Sequence Listing; English.

The present sequence is one of a large number of 5' ESTs derived from
mRNAs encoding secreted proteins. No ORF has yet been conclusively
identified within the present sequence. The 5' ESTs were prepared from
total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
sequences usually correspond mainly to the 3' untranslated region (UTR)
of the mRNA because they are often obtained from oligo-dT primed cDNA
libraries. Such ESTs are not well suited for isolating cDNA sequences
derived from the 5' ends of mRNAs and even in those cases where longer
cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
ESTs are derived from mRNAs with intact 5' ends and can therefore be used
to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
diagnostic, forensic, gene therapy and chromosome mapping procedures.
They are used to obtain upstream regulatory sequences and to design
expression and secretion vectors

Sequence 195 BP; 23 A; 79 C; 58 G; 32 T; 0 U; 3 Other;

Query Match 17.3%; Score 26.6; DB 3; Length 195;

Best Local Similarity 56.2%; Pred. No. 2e+03; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

30 CGAGTCGCGCGCGAGCTGTCATCTCGCTCATCTGTCGAGTGGCGGCGGAGCTCGA 89

DB 134 CGAGCGCGCGCTGAGCTGGAGACGTAGACTTAGGCCGAGCGGAGCGAAGAAATCC 75

QY 90 CGATGACGAGATATACCACTCCGCGCGC 118

DB 74 CGCCGAACGCGAGACACACGCGCGCGCAGC 46

RESULT 29

AA117387

ID AA117387 standard; cDNA; 170 BP.

AA117387;

07-DEC-2001 (first entry)

Human breast cancer expressed polynucleotide 9844.

Human, breast cancer; cell marker; cytosolic; ss.

Homo sapiens.

WO200151628-A2.

19-JUL-2001;

10-JAN-2001; 2001WO-US000798.

14-JAN-2000; 2000US-0176077P.

14-MAR-2000; 2000US-0189167P.

24-MAR-2000; 2000US-0192099P.

29-MAR-2000; 2000US-0193480P.

15-MAY-2000; 2000US-0205230P.

09-JUN-2000; 2000US-0211315P.

25-JUL-2000; 2000US-0220534P.

(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Lillie J, Xu Y, Wang Y, Steinmann K;

WPI; 2001-451856/48.

New peptide useful as a marker for the diagnosis of breast cancer.

Claim 1; Page 1753; 3695pp; English.

The invention relates to human breast cancer expressed polynucleotides
affected with breast cancer by examining the correlation between the
expression of certain markers and the cancerous state of breast cells.
The polynucleotides and encoded polypeptides are potential markers for
detecting, diagnosing, monitoring, characterizing treating and
potentially preventing breast cancer. The polynucleotides and encoded
polypeptides are also useful for isolating compounds with cytostatic
activity

Sequence 170 BP; 25 A; 50 C; 64 G; 31 T; 0 U; 0 Other;

Query Match 16.9%; Score 26; DB 4; Length 170;

Best Local Similarity 55.6%; Pred. No. 2.8e+03; Indels 0; Gaps 0;

Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 61 CATGTCGAGTCGGCGCGCGAGCTCGACGTAGGAGATGACCACTCCGCGCGCG 120

DB 18 CTTGTCGCGCGCGGTCTGTGATGAGCGCGGTGATGATGGGGTGGCTCCGGCGGCA 77

QY 121 ACTGCACTGATGACGAGATGACCACTCCG 150

DB 78 GCTGTCGATCACGACACTTCAGATCGG 107

RESULT 30

AA117387/C

ID AA117387 standard; cDNA; 170 BP.

```
XX AL17387;
AC
XX 07-DEC-2001 (first entry)
DT
XX Human breast cancer expressed polynucleotide 9844.
DE
XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US000798.
PF
XX 14-JAN-2000; 2000US-0176077P.
PR
XX 14-MAR-2000; 2000US-0189167P.
PR
XX 24-MAR-2000; 2000US-0192099P.
PR
XX 29-MAR-2000; 2000US-0193480P.
PR
XX 15-MAY-2000; 2000US-0205230P.
PR
XX 09-JUN-2000; 2000US-0211315P.
PR
XX 25-JUL-2000; 2000US-0220534P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Liilie J, Xu Y, Wang Y, Steinmann K;
PI
XX WPI; 2001-451856/48..
DR
XX New peptide useful as a marker for the diagnosis of breast cancer.
PT
XX Claim 1; Page 1753; 3695pp; English.
PS
XX The invention relates to human breast cancer expressed polynucleotides
CC (AL07544-AL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
CC
XX
XX Sequence 170 BP; 25 A; 50 C; 64 G; 31 T; 0 U; 0 Other;
SQ
Query Match 16.9%; Score 26; DB 4; Length 170;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 5 CGAGCTGTCATCTGCTCATCTGTCAGTCGCGCGCGAGCTGTCATCTGCTCATC 64
DB 107 CCGACTGGAAGTGTGGTGTGATCGACGAGCTGCGCGCGAGCGACGCCCATCTCGCAGC 48
QY 65 GTCCAGTGGCGCGCGCGCGCGACTCCGACGATG 94
DB 47 GCGCCATGACCAAGACCGCGCGCGACGAG 18
```

```
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US000798.
PF
XX 14-JAN-2000; 2000US-0176077P.
PR
XX 14-MAR-2000; 2000US-0189167P.
PR
XX 24-MAR-2000; 2000US-0192099P.
PR
XX 29-MAR-2000; 2000US-0193480P.
PR
XX 15-MAY-2000; 2000US-0205230P.
PR
XX 09-JUN-2000; 2000US-0211315P.
PR
XX 25-JUL-2000; 2000US-0220534P.
XX
XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
PA
XX Liilie J, Xu Y, Wang Y, Steinmann K;
PI
XX WPI; 2001-451856/48.
DR
XX New peptide useful as a marker for the diagnosis of breast cancer.
PT
XX Claim 1; Page 382; 3695pp; English.
PS
XX The invention relates to human breast cancer expressed polynucleotides
CC (AL07544-AL26789) and methods of assessing whether a patient is
CC afflicted with breast cancer by examining the correlation between the
CC expression of certain markers and the cancerous state of breast cells.
CC The polynucleotides and encoded polypeptides are potential markers for
CC detecting, diagnosing, monitoring, characterizing treating and
CC potentially preventing breast cancer. The polynucleotides and encoded
CC polypeptides are also useful for isolating compounds with cytostatic
CC activity
CC
XX
XX Sequence 189 BP; 25 A; 58 C; 74 G; 32 T; 0 U; 0 Other;
SQ
Query Match 16.9%; Score 26; DB 4; Length 189;
Best Local Similarity 55.6%; Pred. No. 2.8e+03;
Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
QY 61 CATGTCGAGTCGCGCGCGCGCGACTGACGATGACGACGATGACGACGCTCCGCGCG 120
DB 33 CTGCTGCGCGCGGTTCTGTCGATGCGCGCGCGACGATGGGCTGCTCGCGCGCA 92
QY 121 ACTGACGATGACGAGATGACCACTCCG 150
DB 93 GCTGTCGATCACCGACACTTCAGTCCG 122
```

RESULT 32
AL09498 standard; CDNA; 189 BP.

```
XX AL09498;
AC
XX 07-DEC-2001 (first entry)
DT
XX Human breast cancer expressed polynucleotide 1955.
DE
XX Human; breast cancer; cell marker; cytostatic; ss.
KM
XX Homo sapiens.
OS
XX WO200151628-A2.
PN
XX 19-JUL-2001.
PD
XX 10-JAN-2001; 2001WO-US000798.
PF
XX 14-JAN-2000; 2000US-0176077P.
PR
XX 14-MAR-2000; 2000US-0189167P.
PR
XX 24-MAR-2000; 2000US-0192099P.
```

29-MAR-2000; 2000US-0193480P.
 PR 15-MAY-2000; 2000US-0205230P.
 PR 09-JUN-2000; 2000US-0211315P.
 PR 25-JUL-2000; 2000US-0220534E.
 XX
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 XX Lillie J, Xu Y, Wang Y, Steinmann K;
 XX WPI; 2001-451856/48.
 XX
 XX New peptide useful as a marker for the diagnosis of breast cancer.
 XX
 XX Claim 1; Page 382; 3695pp; English.
 XX
 CC The invention relates to human breast cancer expressed polynucleotides
 CC (AA107544-AA106788) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterizing, treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity
 CC
 SQ Sequence 189 BP; 25 A; 58 C; 74 G; 32 T; 0 U; 0 Other;
 XX
 XX
 Query Match 16.9%; Score 26; DB 4; Length 189;
 Best Local Similarity 55.6%; Pred. No. 2.8e+03;
 Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;
 OY 5 CGAGCTGATCATCTGCTCATCTGCTGAGTCGCGCGCGAGCTGATCTGCTCATC 64
 DB 122 CGAGCTGATCATCTGCTCATCTGCTGAGTCGCGCGCGAGCTGATCTGCTCATC 63
 OY 65 GTCCAGTGGCGGCGCGCGCGAGCTGCGATG 94
 DB 62 GCGCCATCGACCGAACC GCGCGCGAG 33
 XX
 RESULT 33
 AAT49353
 ID AAT49353 standard; DNA; 183 BP.
 XX
 AC AAT49353;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE N. fischeri internal transcribed spacer 1 sequence.
 XX
 KW Filamentous; fungus; Byssochlamys nivea; Neosartorya fischeri; primer;
 KW Zygosaccharomyces bailii; PCR; amplification; polymerase chain reaction;
 KW ribosomal internal transcribed spacer; detection; heat resistant; fruit;
 KW microorganism; contaminant; strawberry; foodstuff; ss.
 XX
 OS Neosartorya fischeri.
 XX
 PN WO9638587-A2.
 XX
 PD 05-DEC-1996.
 XX
 PF 31-MAY-1996; 96WO-FR000821.
 XX
 PR 02-JUN-1995; 95FR-00006578.
 XX
 PA (UNIR-) UNIR ULTRA PROPRE NUTRITION IND RECH.
 XX
 PI Chrzavetz E, Aufreere R;
 XX WPI; 1997-034393/03.
 XX
 PT Primers derived from internal transcribed spacer sequences - used to
 PT detect contaminants of foodstuffs, esp Byssochlamys nivea, Neosartorya

PT fischeri or Zygosaccharomyces bailii.
 XX
 XX Claim 1; Page 12; 18pp; French.
 XX
 CC The invention relates to methods to detect the filamentous fungi
 CC Byssochlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii by
 CC PCR amplification on genomic DNA using primers derived from the ribosomal
 CC internal transcribed spacer (ITS) sequences (see AAT49351-6). This
 CC sequence represents the ITS1 from N. neosartorya and is amplified by the
 CC primers AAT49359-60. The method is used to detect heat resistant
 CC microorganisms of the above species which are important contaminants of
 CC fruit, especially strawberry-based foodstuffs
 CC
 SQ Sequence 183 BP; 30 A; 62 C; 52 G; 39 T; 0 U; 0 Other;
 XX
 XX
 Query Match 16.6%; Score 25.6; DB 2; Length 183;
 Best Local Similarity 59.7%; Pred. No. 3.5e+03;
 Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
 OY 64 CGTGAATCGGCGCGCGCGAGCTGCGAGTGAACGATGACGCTCCGCGCGACT 123
 DB 67 CGCGTTTCAGCGCGCGCGAGGCTCGCGCGCGCGCGCGCGCGCGAGAC 126
 OY 124 CGACGATGAGCG 135
 DB 127 CCAACATGAAG 138
 XX
 RESULT 34
 AAT49353/C
 ID AAT49353 standard; DNA; 183 BP.
 XX
 AC AAT49353;
 XX
 DT 10-SEP-1997 (first entry)
 XX
 DE N. fischeri internal transcribed spacer 1 sequence.
 XX
 KW Filamentous; fungus; Byssochlamys nivea; Neosartorya fischeri; primer;
 KW Zygosaccharomyces bailii; PCR; amplification; polymerase chain reaction;
 KW ribosomal internal transcribed spacer; detection; heat resistant; fruit;
 KW microorganism; contaminant; strawberry; foodstuff; ss.
 XX
 OS Neosartorya fischeri.
 XX
 PN WO9638587-A2.
 XX
 PD 05-DEC-1996.
 XX
 PF 31-MAY-1996; 96WO-FR000821.
 XX
 PR 02-JUN-1995; 95FR-00006578.
 XX
 PA (UNIR-) UNIR ULTRA PROPRE NUTRITION IND RECH.
 XX
 PI Chrzavetz E, Aufreere R;
 XX WPI; 1997-034393/03.
 XX
 PT Primers derived from internal transcribed spacer sequences - used to
 PT detect contaminants of foodstuffs, esp Byssochlamys nivea, Neosartorya
 PT fischeri or Zygosaccharomyces bailii.
 XX
 PS Claim 1; Page 12; 18pp; French.
 XX
 CC The invention relates to methods to detect the filamentous fungi
 CC Byssochlamys nivea, Neosartorya fischeri and Zygosaccharomyces bailii by
 CC PCR amplification on genomic DNA using primers derived from the ribosomal
 CC internal transcribed spacer (ITS) sequences (see AAT49351-6). This
 CC sequence represents the ITS1 from N. neosartorya and is amplified by the
 CC primers AAT49359-60. The method is used to detect heat resistant
 CC microorganisms of the above species which are important contaminants of
 CC fruit, especially strawberry-based foodstuffs

XX Sequence 183 BP; 30 A; 62 C; 52 G; 39 T; 0 U; 0 Other;
SQ
Query Match 16.6%; Score 25.6; DB 2; Length 183;
Best Local Similarity 59.7%; Pred. No. 3.5e+03;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 20 CGCTCATGTCGAGTCGGCGCGGAGCTGATCTGTCATGTCGTCGAGTCGGCGGC 79
DB 138 CGTTTCATGTTGGGGTCTTTCGGCGGCGCGGCGCGGCGCGGCGCGGCGCTCCCGCGCGCC 79
QY 80 GCCGACTCGACG 91
DB 78 GTCGAAACGGCG 67
RESULT 35
ID AAA94339 standard; DNA; 123 BP.
XX AAA94339;
AC
DT 11-JAN-2001 (first entry)
XX
DE 123-mer DNA PP.01.
XX
KM RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS Synthetic.
XX
PN MO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000MO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 72; 121pp; English.
XX
XX The present sequence was used in a method for generating RNA-protein
CC fusions, which comprise a protein covalently linked to the 3' end of its
CC own mRNA. The fusions are made by synthesis and in vitro or in situ
CC translation of an mRNA molecule with a peptide acceptor attached to its
CC 3' end. The RNA-protein fusions are incubated under high salt conditions
CC to produce a protein library. This method is useful for improving or
CC altering existing proteins, as well as for isolating new proteins and
CC nucleic acid or small molecule targets. It may also be used to improve
CC human or humanised single-chain antibodies for the treatment of a number
CC of diseases. The method is useful for the isolation of proteins with
CC specific binding properties, for screening cDNA libraries and cloning new
CC genes on the basis of protein-protein interactions. Unlike prior art, the
CC new method does not rely on maintaining the integrity of an
CC mRNA:ribosome:nascent chain ternary complex, which is very fragile and is
CC therefore of limited use. The method does not rely on topological links
CC between the protein and the nucleic acid so that the information of the
CC protein is retained and can be recovered in readable, nucleic acid form
XX
SQ Sequence 123 BP; 4 A; 15 C; 8 G; 15 T; 0 U; 81 Other;
XX
Query Match 16.2%; Score 25; DB 3; Length 123;
Best Local Similarity 15.0%; Pred. No. 4.8e+03;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;

Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;
QY 18 CTGCTCATGTCGAGTCGGCGCGGAGCTGATCTGTCATGTCGAGTCGGCGG 77
DB 12 CTGTGATCTSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 71
QY 78 CCGCCGACTCGACGATGAGCGAGATGACGACTCCGCGCGCGGACTC 124
DB 72 NSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 118
RESULT 36
ID AAA94339/c
XX AAA94339;
AC
DT 11-JAN-2001 (first entry)
XX
DE 123-mer DNA PP.01.
XX
KM RNA-protein fusion; protein library; protein isolation; gene cloning; ss.
XX
OS Synthetic.
XX
PN MO200047775-A1.
XX
PD 17-AUG-2000.
XX
PF 01-FEB-2000; 2000MO-US002589.
XX
PR 09-FEB-1999; 99US-00247190.
XX
PA (GENO) GEN HOSPITAL CORP.
XX
PI Szostak JW, Roberts RW, Liu R;
XX
DR WPI; 2000-533022/48.
XX
PT Producing protein or DNA libraries which are useful for improving
PT existing proteins, by in vitro translating protein coding sequences to
PT produce RNA-protein fusions and incubating these protein fusions under
PT high salt conditions.
XX
PS Disclosure; Page 72; 121pp; English.
XX
XX The present sequence was used in a method for generating RNA-protein
CC fusions, which comprise a protein covalently linked to the 3' end of its
CC own mRNA. The fusions are made by synthesis and in vitro or in situ
CC translation of an mRNA molecule with a peptide acceptor attached to its
CC 3' end. The RNA-protein fusions are incubated under high salt conditions
CC to produce a protein library. This method is useful for improving or
CC altering existing proteins, as well as for isolating new proteins and
CC nucleic acid or small molecule targets. It may also be used to improve
CC human or humanised single-chain antibodies for the treatment of a number
CC of diseases. The method is useful for the isolation of proteins with
CC specific binding properties, for screening cDNA libraries and cloning new
CC genes on the basis of protein-protein interactions. Unlike prior art, the
CC new method does not rely on maintaining the integrity of an
CC mRNA:ribosome:nascent chain ternary complex, which is very fragile and is
CC therefore of limited use. The method does not rely on topological links
CC between the protein and the nucleic acid so that the information of the
CC protein is retained and can be recovered in readable, nucleic acid form
XX
SQ Sequence 123 BP; 4 A; 15 C; 8 G; 15 T; 0 U; 81 Other;
XX
Query Match 16.2%; Score 25; DB 3; Length 123;
Best Local Similarity 15.0%; Pred. No. 4.8e+03;
Matches 16; Conservative 26; Mismatches 65; Indels 0; Gaps 0;
QY 31 GAGTCGGCGCGGAGCTGATCTGTCATGTCGAGTCGGCGCGGCGGACTCGAC 90
DB 118 GAGCAAGCGCGAGAGGNNNSNNSNNSNNSNNSNNSNNSNNSNNSNNSN 59

OY 91 GATGAGCGATGACGCTCCGCGCCGACTCGACATGACGAG 137
 Db 58 SNNNSNNNSNNNSNNNSNNNSNNNSNNNSNNNSGATGACAAAG 12

RESULT 37
 ACH88658
 ID ACH88658 standard; DNA; 108 BP.

ACH88658;
 29-JUL-2004 (first entry)

Human genome derived single exon probe #21853.

Human; probe; ss; gene expression; single exon probe; microarray;
 alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386.

(PENN/) PENN S G.

(RANK/) RANK D R.

(HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 21853; 80bp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 688 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, a customer desiring to measure gene expression, a method of providing human gene expression data by subsequence, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterizing alternative splicing events, in detecting and characterizing gross alterations in the genomic locus that includes their exon, in assessing

CC smaller genomic alterations, in printing the synthesis of nucleic acids,
 CC or in expressing the ORF-encoded peptide. The present sequence is a human
 CC single exon probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=20030194704
 CC
 XX Sequence 108 BP; 15 A; 39 C; 34 G; 20 T; 0 U; 0 Other;

Query: Match 16.1%; Score 24.8; DB 12; Length 108;
 Best Local Similarity 72.7%; Pred. No. 5.3e+03;
 Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 106 CAGTCCGCGCCGCGACTCGACATGACGAGATGACGACTCC 149
 Db 5 CTGCTCCTGCGCGCGCTCGCTCGAGCCGAGGAGCCAGCTTC 48

RESULT 38
 ACH88658/c
 ID ACH88658 standard; DNA; 108 BP.

ACH88658;

29-JUL-2004 (first entry)

Human genome derived single exon probe #21853.

Human; probe; ss; gene expression; single exon probe; microarray;
 alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386.

(PENN/) PENN S G.

(RANK/) RANK D R.

(HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 21853; 80bp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 688 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridizes under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above,

CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704
CC
XX Sequence 108 BP; 15 A; 39 C; 34 G; 20 T; 0 U; 0 Other;
SQ
Query Match 16.1%; Score 24.8; DB 12; Length 108;
Best Local Similarity 72.7%; Pred. No. 5.3e+03;
Matches 32; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 6 GGAGCTGCTCATCTGCTCATCTGCTGAGTCCGCGCGGAGCTG 49
Db 48 GAGCTGCTCTCCGCTCCGAGCGAGCGCGCGGAGAGAG 5
RESULT 39
ACD96616
ID ACD96616 standard; cDNA, 130 BP.
XX
AC ACD96616;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #5028.
XX
XX Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX US2002155438-A1.
PN
XX 24-OCT-2002.
PD
XX 27-SEP-1999; 99US-00406117.
PF
XX 20-NOV-1998; 98US-00196716.
PR
XX (STMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
XX Simpson AJG, Neto ED, Brentani RR;
PI
XX WPI; 2003-182626/18.
DR
XX
XX Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
XX Example 9; Page 721; 959pp; English.
PS
XX The invention describes a method of determining open reading frames in

CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (I), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing resulting
CC nucleic acids. The method is useful for determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig,
CC nucleic acid molecule from a genome of an organism, and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as
CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX
SQ Sequence 130 BP; 28 A; 44 C; 35 G; 23 T; 0 U; 0 Other;
XX
Query Match 16.1%; Score 24.8; DB 10; Length 130;
Best Local Similarity 57.9%; Pred. No. 5.4e+03;
Matches 44; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
OY 71 TGGCGCGCGCGGAGCTGAGCATGAGGAGTACCAAGCTCCGCCGAGCTGACGAT 130
Db 26 TGGCGGAGGAGGAGGCTTAAACATGACGACGACCTTGAACCGCTGACGACCAT 85
OY 131 GAGCGAGATGACGACG 146
Db 86 CTTGAGCTGACCTGC 101
RESULT 40
ACD96616/c
ID ACD96616 standard; cDNA, 130 BP.
XX
AC ACD96616;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #5028.
XX
XX Open reading frame detection; genome sequencing; colon cancer;
KW breast cancer; population genome analysis; genetic shift; cancer;
KW antibiotic resistance; antibiotic non-tolerance; congenital disease;
KW agriculture; food crop genome; resistance gene; retrovirus;
KW influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KW gene; ss.
XX
XX Homo sapiens.
OS
XX US2002155438-A1.
PN
XX 24-OCT-2002.
PD
XX 27-SEP-1999; 99US-00406117.
PF
XX

PF 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GENSET) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 16612; 71pp + Sequence listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNA or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX cDNA sequences have been obtained, the full 5' UTR is rarely included. 5'
XX ESTs are derived from mRNAs with intact 5' ends and can therefore be used
XX to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX They are used to obtain upstream regulatory sequences and to design
XX expression and secretion vectors
XX
XX Sequence 181 BP; 35 A; 35 C; 92 G; 19 T; 0 U; 0 Other;
XX
XX
XX Query Match 16.1%; Score 24.8; DB 3; Length 181;
XX Best Local Similarity 67.3%; Pred. No. 5.4e+03;
XX Matches 35; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
XX
XX 79 CGCGGATCGACGATGACGAGACGAGCTCGGCGCGGATCGACGAT 130
XX Db 71 CGCGCGCGCGGAGAGCCAGACGCTCGCGCGCGCGGAGAGGAGT 20
XX
XX
XX RESULT 43
XX ADS69652
XX ID ADS69652 standard; cDNA; 164 BP.
XX
XX ADS69652;
XX
XX 18-NOV-2004 (first entry)
XX
XX
XX Corn seedling-derived polynucleotide (cpds), SEQ ID 4668.
XX
XX
XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
XX seed development; disease resistance; insect infestation; fungal disease;
XX bacterial infection; Goss' Bacterial wilt; blight;
XX Stewart's bacterial wilt; Holcus spot; bacterial leaf blight; leaf spot;
XX bacterial stripe; maize dwarf mosaic virus infection;
XX environmental stress; water stress; pH stress; temperature stress;
XX pollution; injury; pesticide.
XX
XX
XX Zea mays.
XX
XX US2003237110-A9.
XX
XX 25-DEC-2003;
XX
XX 06-AUG-2001; 2001US-00923876.
XX
XX 12-MAY-1998; 98US-0085331P.
XX 21-APR-1999; 99US-00298329.
XX
XX (INCY-) INCYTE PHARM INC.
XX

PI Lalgudi RV, Ito LY, Sherman BK;
XX
XX WPI; 2002-195165/25.
XX
XX
XX New corn seedling-derived polynucleotides and polypeptides, useful in
XX identifying and altering desired characteristics associated with growth
XX and development, disease resistance, environmental adaptability, quality
XX
XX
XX Claim 1; SEQ ID NO 4668; 33pp; English.
XX
XX
XX The invention relates to a corn seedling-derived polynucleotide (cdp)
XX selected from ADS64985-ADS71316, or their complements and fragments. Also
XX included are a composition for the detection of altered expression of a
XX cdp (comprising a polynucleotide selected from ADS64985-ADS71316), a
XX method of detecting a polynucleotide in a biological sample using a cdp,
XX a method for using oligomers (and amplification) to recover a regulatory
XX element from a DNA library using oligomers designed against a cdp, a
XX seedling specific regulatory element that regulates the expression of a
XX cdp, an expression vector containing a cdp or regulatory element, a plant
XX transformed with the vector, a host cell containing the vector (and
XX expressing a corn seedling derived protein, CDP), an anti-CDP antibody,
XX identifying a compound which binds a CDP and screening a plurality of
XX compounds for binding to cdp polynucleotide. The cdp polynucleotides,
XX proteins, vectors, cells and antibodies are useful for the
XX identification, evaluation and alteration of seed growth and development,
XX disease resistance (e.g. to insect infestation, fungal disease, bacterial
XX infection, Goss' Bacterial wilt, blight, Stewart's bacterial wilt, Holcus
XX spot, bacterial leaf blight, leaf spot, bacterial stripe and maize dwarf
XX mosaic virus infection) and resistance to environmental stress (e.g.
XX water stress, pH stress, temperature stress, pollution, injury or
XX pesticides. The present sequence is cdp cDNA sequence.
XX
XX
XX Sequence 164 BP; 28 A; 53 C; 38 G; 44 T; 0 U; 1 Other;
XX
XX
XX Query Match 15.8%; Score 24.4; DB 7; Length 164;
XX Best Local Similarity 60.6%; Pred. No. 6.7e+03;
XX Matches 40; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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XX 22 CTCATCTCGATGCGCGCGCGAGCTGTGATCTCCTCATCTCGAGTGGCGCGC 81
XX Db 74 CTCGACGACGATGCGGAGCGGAGTGTGGGATCTGCTGCTGCGCCCTTGGCATTT 133
XX
XX
XX 82 CGATCT 87
XX Db 134 CTTCTC 139
XX
XX
XX RESULT 44
XX ADS69652/C
XX ID ADS69652 standard; cDNA; 164 BP.
XX
XX ADS69652;
XX
XX 18-NOV-2004 (first entry)
XX
XX
XX Corn seedling-derived polynucleotide (cpds), SEQ ID 4668.
XX
XX
XX Corn; seedling-derived polynucleotide; cdp; ss; plant; seed growth;
XX seed development; disease resistance; insect infestation; fungal disease;
XX bacterial infection; Goss' Bacterial wilt; blight;
XX Stewart's bacterial wilt; Holcus spot; bacterial leaf blight; leaf spot;
XX bacterial stripe; maize dwarf mosaic virus infection;
XX environmental stress; water stress; pH stress; temperature stress;
XX pollution; injury; pesticide.
XX
XX
XX Zea mays.
XX
XX US2003237110-A9.
XX
XX 25-DEC-2003;
XX
XX 06-AUG-2001; 2001US-00923876.
XX

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:58:47 ; Search time 1842 Seconds
(without alignments)
4051.088 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154
Sequence: 1 cgcgcgcagctgcgtcatctc.....gagatgacacagctccgcgcg 154

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 2422767955 residues

Total number of hits satisfying chosen parameters: 2805242

Minimum DB seq length: 0
Maximum DB seq length: 200

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_bcg:*
3: gb_in:*
4: gb_om:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_stg:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	6	AX367128 Sequence
2	154	100.0	154	6	AX367128 Sequence
3	154	100.0	154	6	AX392336 Sequence
4	154	100.0	154	6	AX392336 Sequence
5	80	51.9	80	6	AX367127 Sequence
6	80	51.9	80	6	AX367127 Sequence
7	80	51.9	80	6	AX392335 Sequence
8	80	51.9	80	6	AX392335 Sequence
9	80	51.9	80	6	AX367129 Sequence
10	80	51.9	80	6	AX367129 Sequence
11	29.4	19.1	194	6	AX047784 Sequence
12	29.4	19.1	194	6	AX047784 Sequence
13	28	18.2	197	6	AR251294 Sequence
14	28	18.2	197	6	AR251294 Sequence
15	27.2	17.7	191	8	AFU557755 Aspergill
16	27.2	17.7	191	8	AFU557755 Aspergill
17	26.6	17.3	156	6	AX393064 Sequence
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C 21	26.6	17.3	190	6	AX393057
C 22	26.6	17.3	190	6	AX393057
C 23	26.6	17.3	195	6	AX898116
C 24	26.6	17.3	195	6	AX898116
C 25	26.6	17.3	195	6	BD033649
C 26	26.6	17.3	195	6	BD033649
C 27	26.2	17.0	171	6	AR427779
C 28	26.2	17.0	171	6	AR427779
C 29	26.2	17.0	171	6	AX988473
C 30	26.2	17.0	171	6	AX988473
C 31	26.2	17.0	171	6	BD123332
C 32	26.2	17.0	171	6	BD123332
C 33	26.2	17.0	170	6	BD123332
C 34	26.2	16.9	170	6	BD123332
C 35	26.2	16.9	170	6	BD123332
C 36	26.2	16.9	189	6	BD123332
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C 38	25.6	16.6	183	6	BD123332
C 39	25.6	16.6	183	6	BD123332
C 40	25.6	16.6	183	6	BD123332
C 41	25.4	16.5	105	5	ALU33657
C 42	25.4	16.5	105	5	ALU33657
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C 44	25.4	16.5	165	1	AB164173
C 45	25.4	16.5	123	6	BD238411
C 46	25.4	16.5	123	6	BD238411
C 47	25.4	16.5	123	6	BD238411
C 48	25.4	16.5	189	1	AY271325
C 49	25.4	16.5	189	1	AY271325
C 50	25.4	16.5	189	1	AY271340
C 51	24.8	16.1	181	6	AX900749
C 52	24.8	16.1	181	6	AX900749
C 53	24.8	16.1	181	6	BD036282
C 54	24.8	16.1	181	6	BD036282
C 55	24.8	16.1	182	14	AY340988
C 56	24.8	16.1	182	14	AY340988
C 57	24.8	16.1	195	6	CQ739774
C 58	24.8	16.1	195	6	CQ739774
C 59	24.4	15.8	185	6	CQ081614
C 60	24.4	15.8	185	6	CQ081614
C 61	24.4	15.8	185	6	CQ081614
C 62	24.4	15.8	185	6	CQ081614
C 63	24.4	15.8	185	6	CQ081614
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C 66	24.4	15.8	185	6	CQ081614
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C 74	24.4	15.8	185	6	CQ081614
C 75	24.4	15.8	185	6	CQ081614
C 76	24.4	15.8	185	6	CQ081614
C 77	24.2	15.7	126	4	BTLFCET52
C 78	24.2	15.7	126	4	BTLFCET52
C 79	24.2	15.7	175	6	AR481853
C 80	24.2	15.7	175	6	AR481853
C 81	24.2	15.7	175	6	AR481853
C 82	24.2	15.7	175	6	AR481853
C 83	24.2	15.7	175	6	AR481853
C 84	24.2	15.7	175	6	AR481853
C 85	24.2	15.7	175	6	AR481853
C 86	24.2	15.7	175	6	AR481853
C 87	24.2	15.7	175	6	AR481853
C 88	23.8	15.5	98	1	RCAPKXA
C 89	23.8	15.5	98	1	RCAPKXA
C 90	23.8	15.5	165	9	AF279907
C 91	23.8	15.5	165	9	AF279907
C 92	23.8	15.5	193	9	AF279906

93 23.6 15.3 71 6 AX899886 Sequence
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94 23.6 15.3 71 6 BD035419 Sequence
c 96 23.6 15.3 71 6 BD035419 Sequence
97 23.6 15.3 171 6 CQ725345 Sequence
c 98 23.6 15.3 171 6 CQ725345 Sequence
99 23.2 15.1 101 11 BV167402 Sequence
c 100 23.2 15.1 101 11 BV167402 Sequence

ALIGNMENTS

RESULT 1
AX367128
LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
Location/Qualifiers

FEATURES
source
1..154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 1 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
QY 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 120
DB 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 120
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 154
DB 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 154

RESULT 2

AX367128/c
LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 13 from Patent WO0200904.
ACCESSION AX367128
VERSION AX367128.1 GI:18855329
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE

AUTHORS
TITLE
JOURNAL
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
Location/Qualifiers

FEATURES

source

1..154
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 154 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 95
QY 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 120
DB 94 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 35
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 154
DB 34 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 1

RESULT 3

AX392336
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE

AUTHORS

Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
Nucleotide sequences of a new class of diverged delta-9
stearoyl-aop desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
Location/Qualifiers

JOURNAL

FEATURES

source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
DB 1 CGGCGGAGCTGGTATCTCGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
QY 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 120
DB 61 CATGTCGAGTCGGCGCGGCGGAGTCGAGTGAACCAAGCTCCGGCGCGCG 120
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 154
DB 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCGCG 154

RESULT 4

AX392336/c
LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 25 from Patent WO0216565.
ACCESSION AX392336
VERSION AX392336.1 GI:19700689
KEYWORDS
SOURCE
synthetic construct

FEATURES

ORGANISM

synthetic construct
other sequences; artificial sequences.

REFERENCE

1 Booth,J.R., Cahoon,R.E., Hitz,W.D., Kinney,A.J. and Yadav,N.S.
Nucleotide sequences of a new class of diverged delta-9

stearoyl-acp desaturase genes
Patent: WO 0216565-A 25 28-FEB-2002;

E. I. du Pont de Nemours and Company (US)

FEATURES

source

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/db_xref="taxon:32630"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.1e-19;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 60

Db

154 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 95

QY

61 CATGTCAGTCGGCGCGCGGAGCTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 120

Db

94 CATGTCAGTCGGCGCGCGGAGCTGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC 35

QY

121 ACTGACGATGACGACGATGACGACGCTCCGCGCG 154

Db

34 ACTGACGATGACGACGATGACGACGCTCCGCGCG 1

RESULT 5

AX367127

LOCUS AX367127 80 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 12 from Patent WO0200904.

ACCESSION AX367127

VERSION AX367127.1 GI:18855328

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

QY

RESULT 6

AX367127/c

LOCUS AX367127 80 bp DNA linear PAT 16-FEB-2002

DEFINITION Sequence 12 from Patent WO0200904.

ACCESSION AX367127

VERSION AX367127.1 GI:18855328

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

QY

Db

RESULT 7

AX392335

LOCUS AX392335 80 bp DNA linear PAT 23-MAR-2002

DEFINITION Sequence 24 from Patent WO0216565.

ACCESSION AX392335

VERSION AX392335.1 GI:19700688

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

ORIGIN

Query Match

Best Local Similarity

Matches

QY

Db

QY

Db

DB	61	GAGATGACCGACTCCGGCGC	80
RESULT 8			
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LOCUS		80 bp	DNA
DEFINITION		Sequence 24 from Patent WO0216565.	linear
AX392335			PAT 23-MAR-2002
ACCESSION			
VERSION			
KEYWORDS		AX392335.1 GI:19700688	
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		1	
TITLE		Booth, J.R., Cahoon, R.E., Hiltz, W.D., Kinney, A.J., and Yadav, N.S.	
JOURNAL		Nucleotide sequences of a new class of diverged delta-9	
		stearoyl-ACP desaturase genes	
		Patent: WO 0216565-A 24 28-FEB-2002;	
		E. I. du Pont de Nemours and Company (US)	
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QY			
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DB	CGCCCGAGCTGTCATCTCGCTCATCTGTCAGTGCAGTGCAGCGCCCGCAGCTGCAGCATGAGC	21	
QY			
98	GAGATGACCGACTCCGGCGC	117	
DB	GAGATGACCGACTCCGGCGC	1	
RESULT 9			
AX367129			
LOCUS		92 bp	DNA
DEFINITION		Sequence 14 from Patent WO0200904.	linear
AX367129			PAT 16-FEB-2002
ACCESSION			
VERSION		AX367129.1 GI:18855330	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS		1	
TITLE		Glaesman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L.	
JOURNAL		and Nichols, S.E.	
		Recombinant constructs and their use in reducing gene expression	
		Patent: WO 0200904-A 14 03-JAN-2002;	
		E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED	
FEATURES		INTERNATIONAL, INC. (US)	
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9y	98	GAGATGACCGAGCTCCGGCCG	117	
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DEFINITION	Sequence 14 from Patent WO0200904.	92 bp	DNA	linear
ACCESSION	AX367129			PAT 16-FEB-2002
VERSION	AX367129.1	GI:18855330		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1			
TITLE	Glasseman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.			
JOURNAL	and Nichols,S.E.			
	Recombinant constructs and their use in reducing gene expression			
	Patent: WO 0200904-A 14 03-JAN-2002;			
	E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED			
	INTERNATIONAL, INC. (US)			
FEATURES				
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9y	98	GAGATGACCGAGCTCCGGCCG	117	
Db	26	GAGATGACCGAGCTCCGGCCG	7	
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DEFINITION	Sequence 16 from Patent WO0070044.	194 bp	DNA	linear
ACCESSION	AX047784			PAT 15-DEC-2000
VERSION	AX047784.1	GI:11876790		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	1			
TITLE	Mittman,S.T. and Agnew,W.S.			
JOURNAL	Human brain c calcium channel alpha-subunit splice variants			
	Patent: WO 0070044-A 16 23-NOV-2000;			
	The Johns Hopkins University (US)			
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9y	30	CGAGTCGGCGCGGAGCTGTCATCTGCTCATGTCGTGAGTCGGGCGCGCGAGTCGA	89	

Db 22 CGAGCTGCGGAGAGCGCTGCGCGCTCTCATCATCCAGCGCGCGACACCATGT 81
Qy 90 CGATGAGCGAGATATCCAGCTCCGCC 116
Db 82 CGTGCCCAAGAGCAGCAGCGGCC 108

RESULT 12
AX047784/c
LOCUS AX047784 194 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 16 from Patent WO070044.
ACCESSION AX047784
VERSION AX047784.1 GI:11876790
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Miltman,S.T. and Agnew,W.S.
TITLE Human brain c calcium channel alpha-subunit splice variants
JOURNAL Patent: WO 0070044-A 16 23-NOV-2000;
The Johns Hopkins University (US)
FEATURES
source location/Qualifiers
1. 194
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Best Local Similarity 58.6%; Pred. No. 4.1e+04;
Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Db 108 GCGCGAGCTGTCATCTCGCTCATCTGTCAGTCGCGCGCGCGACTCGAGTGAAGCG 49
Qy 99 AGATGACCAAGCTCCGCGCGCGACTCG 125
Db 48 GCGCGAGCAGGCTCTCGCAGCTCCG 22

RESULT 13
AR251294
LOCUS AR251294 197 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6653 from patent US 6476212.
ACCESSION AR251294
VERSION AR251294.1 GI:27299168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 197)
AUTHORS Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 6653 05-NOV-2002;
location/Qualifiers
1. 197
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 18.2%; Score 28; DB 6; Length 197;
Best Local Similarity 51.2%; Pred. No. 7.6e+04;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 28 GTCAGTCGCGCGCGCGAGCTGTCATCTCGCTCATCTGTCAGTCGCGCGCGCGACTC 87
Db 63 GCGCGAGTCGCGCGCGAGTCGCTCTGCGCGCGAGCAGCTGTACNTCTCTCAGTCTC 122
Qy 88 GACATGACGAGTGAACCAAGCTCCGCGCGCGCGACTCGACATGAGCAGATGACAGCT 147

Db 123 AGTCAGAGCAATGAGTGGTCGCGCGCGAGATGACCGAGAGAGCGGAGAGCAGGA 182
Qy 148 CCGGC 152
Db 183 GCAGC 187

RESULT 14
AR251294/c
LOCUS AR251294 197 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 6653 from patent US 6476212.
ACCESSION AR251294
VERSION AR251294.1 GI:27299168
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 197)
AUTHORS Lalgudi,R.V., Ito,L.Y. and Sherman,B.K.
TITLE Polynucleotides and polypeptides derived from corn ear
JOURNAL Patent: US 6476212-A 6653 05-NOV-2002;
location/Qualifiers
1. 197
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 18.2%; Score 28; DB 6; Length 197;
Best Local Similarity 51.2%; Pred. No. 7.6e+04;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 3 GCGCGAGCTGTCATCTCGCTCATCTGTCAGTCGCGCGCGCGAGCTGTCATCTGCTCA 62
Db 187 GCTGCTCTCTCTCTCCGCTCTCTCTGTCATCTGCGCGCGCACCATCTTGTCTCC 128
Qy 63 TCGTCAGTCGCGCGCGCGCGAGCTCGAGTGAAGCAGATGACCGCTCGCGCGCGAGC 122
Db 127 TGACTGAGACTGAGAGAGAGTAAACAGCTGCGCGCGAGAGATTCGGCGGACACC 68
Qy 123 TCGAC 127
Db 67 GCGGC 63

RESULT 15
AFU557755
LOCUS AFU557755 191 bp DNA linear PLN 19-APR-2004
DEFINITION Aspergillus fumigatus ITS1, isolate 8.
ACCESSION AFU557755
VERSION AFU557755.1 GI:46406330
KEYWORDS Internal transcribed spacer 1; ITS1.
SOURCE Aspergillus fumigatus
ORGANISM Aspergillus fumigatus
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.

REFERENCE
AUTHORS Hain,M.
TITLE Detection and identification of fungi from bryozoa
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 191)
AUTHORS Hain,M.
TITLE Direct Submission
JOURNAL Submitted (18-APR-2003) Hain M., ICBM, Carl v. Ossietzky
Universitaet Oldenburg, C. v. O. Strasse 9-11, D-26111 Oldenburg,
GERMANY
location/Qualifiers
1. 191
/organism="Aspergillus fumigatus"
/mol_type="genomic DNA"
/isolate="8"
/specific_host="Alcyonidium gelatinosum"
/db_xref="taxon:5085"
/country="Germany:North Sea around the island of

VERSION	ABI64172.2	GI:45421893
KEYWORDS		
SOURCE	uncultured bacterium	

Department of Urban Engineering; 7-3-1, Hongo, Bunkyo, Tokyo 113-8656, Japan (E-mail: shoji@env.t.u-tokyo.ac.jp, Tel: 81-3-5841-7784, Fax: 81-3-5841-8538)
 On Mar 13, 2004 this sequence version replaced gi:45330784.

COMMENT
 FEATURES
 source

1. 165
 /organism="uncultured bacterium"
 /mol_type="genomic DNA"
 /isolate="DGSR Band F215-Ko"
 /isolation_source="activated sludge from lab-scale SBR fed with wastewater"
 /db_xref="taxon:77133"
 /environmental_sample
 /country="Japan;Tokyo"
 /note="PCR products amplified by primers nirs2fGC and nirs3R were analyzed by DGGE"

gene
 1. 165
 /gene="nirs"
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 /gene="nirs"
 /codon_start=1
 /transl_table=1
 /product="nitrite reductase"
 /protein_id="BA012410.2"
 /db_xref="GI:45421894"
 /translation="YHPEPRVASIVASHSPFVYVNYKETGLMDYSINDALKTEIGSRFLHDDG"

ORIGIN

Query Match 17.3%; Score 26.6; DB 1; Length 165;
 Best Local Similarity 56.2%; Pred. No. 1,4e+05;
 Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Oy 24 CATCGTCGAGTCGGCGCGCGAGCTGTGTCATCTCGTCATCGTCGAGTCGGCGCGCG 83
 |||||
 Db 160 CGTCGTCAAGAGCGCGCGCGAGCTGTGTCATCTCGTCATCGTCGAGTCGGCGCGCG 101
 |||||

Oy 84 ACTGCACATGAGCGAGATGACCACTCC 112
 |||||
 Db 100 AGTCGACCATCAGCGCTGTGCGCGCTCC 72
 |||||

RESULT 21
 AX393057
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1
 Koesia,S.
 Regulation of human glutamate receptor delta-1 subunit
 Patent: WO 0206313-A 2 24-JAN-2002;
 Bayer Aktiengesellschaft (DB)
 location/Qualifiers
 1. 190
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

FEATURES
 source

ORIGIN

Query Match 17.3%; Score 26.6; DB 6; Length 190;
 Best Local Similarity 60.3%; Pred. No. 1,4e+05;
 Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Oy 60 TCATCGTCGAGTCGGCGCGCGCGACTCGAGATGAGCGAGATGACCACTCGCGCGCGCC 119
 |||||
 Db 20 TCCTCGAGAGAACCGCGCGCGCAAGACGACGAGGTCTTCCAGTTGGCGGTATCCGACCTGA 79
 |||||

QY 120 GACTCGACGATGA 132
Db 80 GCCTCAACGATGA 92

RESULT 22
AX393057/c 190 bp DNA linear PAT 23-MAR-2002
LOCUS Sequence 2 from Patent WO206313.
DEFINITION AX393057
ACCESSION AX393057
VERSION AX393057.1 GI:19701113
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Kossida, S.
TITLE Regulation of human glutamate receptor delta-1 subunit
JOURNAL Patent: WO 0206313-A 2 24-JAN-2002;
Bayer Aktiengesellschaft (DE)
FEATURES
source location/Qualifiers
1..190
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.3%; Score 26.6; DB 6; Length 190;
Best Local Similarity 60.3%; Pred. No. 1.4e+05;
Matches 44; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 23 TCATCTGTCGAGTCGCGCGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGCGG 82
Db 92 TCATCTGTCGAGTCGCGCGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGG 33
QY 83 GACTCGACGATGA 95
Db 32 TTCTCTCTGAGAGA 20

RESULT 23
AX898116 195 bp DNA linear PAT 18-DEC-2003
LOCUS AX898116
DEFINITION Sequence 13979 from Patent EP1033401.
ACCESSION AX898116
VERSION AX898116.1 GI:40053029
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclet, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 13979 06-SEP-2000;
Genet (FR)
FEATURES
source location/Qualifiers
1..195
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.3%; Score 26.6; DB 6; Length 195;
Best Local Similarity 56.2%; Pred. No. 1.4e+05;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 37 GCGGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGCGGAGTCGACGATGAG 96
Db 46 GCTGCGCGCGGCTGTCGCTGTCGCGCGGAGTCCTTCTGCTCGGCTCGGCTTAACT 105
QY 97 CGAGATGACGAGCTCGGCGCGGAGTCG 125

Db 106 CTAAGTCCCGAGCTCCAGCGCGGCTCG 134

RESULT 24
AX898116 195 bp DNA linear PAT 18-DEC-2003
LOCUS AX898116
DEFINITION Sequence 13979 from Patent EP1033401.
ACCESSION AX898116
VERSION AX898116.1 GI:40053029
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Dumas Milne Edwards, J.B., Duclet, A. and Giordano, J.Y.
TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 13979 06-SEP-2000;
Genet (FR)
FEATURES
source location/Qualifiers
1..195
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.3%; Score 26.6; DB 6; Length 195;
Best Local Similarity 56.2%; Pred. No. 1.4e+05;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 30 CGAGTCGCGCGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGCGGAGTCGA 89
Db 134 CGAGTCGCGCGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGCGGAGTCGA 75
QY 90 CGATGACGAGATGACGAGCTCGCGCGG 118
Db 74 CGCCGAGCGGAGGACGAGCTCGCGGAGC 46

RESULT 25
BD033649 195 bp DNA linear PAT 27-AUG-2002
LOCUS BD033649
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD033649
VERSION BD033649.1 GI:22575391
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Edwards, J.B.D.M., Duclet, A. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 9895 02-OCT-2001;
GENSET
COMMENT
OS Homo sapiens (human)
PN JP 2001269182-A/9895
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC

FEATURES
source location/Qualifiers
1..195
/organism="Homo sapiens"
/mol_type="genomic DNA"

ORIGIN /db_xref="taxon:9606"

Query Match 17.3%; Score 26.6; DB 6; Length 195;
Best Local Similarity 56.2%; Pred. No. 1.4e+05;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 37 GCGGCCGAGCTGGTCTGCTCATCTGAGTCGCGCGCCGCGACTGAG 96
Db 46 GCTGCGCGCGGCTGTCTGCGGATTTCTTCTGCTGCGCTGCGCTAGT 105

Qy 97 CGAGATGACGAGCTCCGCGCGCGACTCG 125
Db 106 CTACGTCCTCCGAGCTCCAGCCGCGGCTCG 134

RESULT 26
BD033649/c 195 bp DNA linear PAT 27-AUG-2002
LOCUS
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD033649
VERSION BD033649.1 GI:22575391
KEYWORDS JP 2001269182-A/9895.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 195)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 9895 02-OCT-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/9895
PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
PI JORDAN
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68//G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40

FEATURES
source Location/Qualifiers
1..195
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 17.3%; Score 26.6; DB 6; Length 195;
Best Local Similarity 56.2%; Pred. No. 1.4e+05;
Matches 50; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 30 CGAGTCGCGCGCGAGCTGCTCATCTGCTCATCTGAGTCGCGCGCCGCGACTGGA 89
Db 134 CGAGTCGCGCGCGAGCTGCTCATCTGCTCATCTGAGTCGCGCGCCGCGACTGGA 75

Qy 90 CGATGAGGAGATGACGAGCTCCGCGCGC 118
Db 74 CGCGGACGCGAGACACGCTCCGCGCAGC 46

RESULT 27
AR427779 171 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 19276 from patent US 6639063.
ACCESSION AR427779
VERSION AR427779.1 GI:40182889
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 171)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 19276 28-OCT-2003;
FEATURES
source Location/Qualifiers
1..171
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 37 GCGGCCGAGCTGGTCTGCTCATCTGAGTCGCGCGCCGCGACTGAG 96
Db 47 GCTGCGCGCGGCTGTCTGCGGATTTCTTCTGCTGCGCTGCGCTAGT 106

Qy 97 CGAGATGACGAGCTCCGCGCGCGACTCG 125
Db 107 CTACGTCCTCCGAGCTCCAGCCGCGGACTCG 135

RESULT 28
AR427779/c 171 bp DNA linear PAT 18-DEC-2003
LOCUS
DEFINITION Sequence 19276 from patent US 6639063.
ACCESSION AR427779
VERSION AR427779.1 GI:40182889
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 171)
AUTHORS Edwards, J.B.D.M., Jobert, S. and Giordano, J.-Y.
TITLE EST's and encoded human proteins
JOURNAL Patent: US 6639063-A 19276 28-OCT-2003;
FEATURES
source Location/Qualifiers
1..171
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 30 CGAGTCGCGCGCGAGCTGCTCATCTGCTCATCTGAGTCGCGCGCCGCGACTGGA 89
Db 135 CGAGTCGCGCGCGAGCTGCTCATCTGCTCATCTGAGTCGCGCGCCGCGACTGGA 76

Qy 90 CGATGAGGAGATGACGAGCTCCGCGCGC 118
Db 75 CGCGGACGCGAGACACGCTCCGCGCAGC 47

RESULT 29
AX988473 171 bp DNA linear PAT 15-JAN-2004
LOCUS
DEFINITION Sequence 19276 from Patent EP104808.
ACCESSION AX988473
VERSION AX988473.1 GI:40994650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
TITLE ESTs and encoded human proteins
JOURNAL Patent: EP 1104808-A 19276 06-JUN-2001;

FEATURES
source
Genset (FR)
Location/Qualifiers
1..171
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 37 GCGGCCGAGCTGTGTCATCTCGCTCATCTGAGTCGCGCGCGCGAGCTGAGATAG 96
Db 47 GCTCGCGCGCGCGGTCTCTCGGTCGCGGAGATTCTTCTGCTCGGCTCGGCTTAGT 106
Qy 97 CGAGATGACCACTTCGCGCGCGCGACTCG 125
Db 107 CTACGTCCCGACCTCCAGCCCGCGGTCG 135

RESULT 30
AX988473/c 171 bp DNA linear PAT 15-JAN-2004
LOCUS AX988473
DEFINITION Sequence 19276 from Patent Epi104808.
ACCESSION AX988473
VERSION AX988473.1 GI:40994650
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.E.
ESTs and encoded human proteins
Patent: EP 1104808-A 19276 06-JUN-2001;
Genset (FR)
Location/Qualifiers
1..171
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source
Genset (FR)
Location/Qualifiers
1..171
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 30 CGAGTCGCGCGCGAGCTGTGTCATCTCGCTCATCTGAGTCGCGCGCGCGACTCGA 89
Db 135 CGAGTCGCGCGCGAGCTGTGTCATCTCGCTCATCTGAGTCGCGCGCGCGACTCGA 76
Qy 90 CGATGAGCGAGATACCACTTCGCGCGCG 118
Db 75 CGCGAAGCGAGACACCGCGCGCGAGC 47

RESULT 31
BD123332 171 bp DNA linear PAT 18-SEP-2002
LOCUS BD123332
DEFINITION EST and encoded human protein.
ACCESSION BD123332
VERSION BD123332.1 GI:23218277
KEYWORDS JP 2002010789-A/15409.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 15409 15-JAN-2002;
GENSET CORP

ORIGIN

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/15409
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PI 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..171
/organism="Homo sapiens (human)".

FEATURES
source
Location/Qualifiers
1..171
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 17.0%; Score 26.2; DB 6; Length 171;
Best Local Similarity 55.1%; Pred. No. 1.7e+05;
Matches 49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;

Qy 37 GCGGCCGAGCTGTGTCATCTCGCTCATCTGAGTCGCGCGCGCGAGCTGAGATAG 96
Db 47 GCTCGCGCGCGCGGTCTCTCGGTCGCGGAGATTCTTCTGCTCGGCTCGGCTTAGT 106
Qy 97 CGAGATGACCACTTCGCGCGCGCGACTCG 125
Db 107 CTACGTCCCGACCTCCAGCCCGCGGTCG 135

RESULT 32
BD123332/c 171 bp DNA linear PAT 18-SEP-2002
LOCUS BD123332
DEFINITION EST and encoded human protein.
ACCESSION BD123332
VERSION BD123332.1 GI:23218277
KEYWORDS JP 2002010789-A/15409.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.
EST and encoded human protein
Patent: JP 2002010789-A 15409 15-JAN-2002;
GENSET CORP

COMMENT OS Homo sapiens (human)
PN JP 2002010789-A/15409
PD 15-JAN-2002
PF 07-AUG-2000 JP 2000280989
PI 05-AUG-1999 US 60/147499
PI JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE
GIORDANO
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12P21/08, C12Q1/68, C12N15/00, C12N5/00, PC
C12N15/00
CC EST and encoded human protein
FH Key Location/Qualifiers
FT source 1..171
/organism="Homo sapiens (human)".

FEATURES
source
Location/Qualifiers
1..171
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN

	Query Match	17.0%; Score 26.2; DB 6;	Length 171;	
	Best Local Similarity	55.1%; Pred. No. 1.7e+05;		
	Matches	49; Conservative 1; Mismatches 39; Indels 0; Gaps 0;		
Qy	30 CGAGTCGGCGGCGCGAGCTGTGCATCTTGCATCATGTGAAGTCGAGCGGCCGACCTGCA	89		
Dd	135 CGAKCCGGCGGCTGGAGCTGGGGAGCTGAGACTTGAGCCGAGCCGAGCGAAGAGAATTCC	76		
Db	90 CGATGAGCGAGATGACCAGCTCCGGCCGC	118		
	75 GC CGGAACGCGAGACACCGCCGCGCACG	47		
RESULT 33				
LOCUS	CQ424819	170 bp	DNA	linear PAT 28-JAN-2004
DEFINITION	Sequence 9853 from Patent WO0151628.			
ACCESSION	CQ424819			
VERSION	CQ424819.1 GI:41377048			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.			
TITLE	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 9853 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)			
JOURNAL	Location/Qualifiers			
FEATURES	1..170			
Source	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"			
ORIGIN				
Query Match	16.9%; Score 26; DB 6; Length 170;			
Best Local Similarity	55.6%; Pred. No. 1.9e+05;			
Matches	50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;			
Qy	61 CATGTCGAGTCGGCGCGCCGCGCAGTCGACGATGAGCGAGTGCACGACTCGGCGCCGC	120		
Dd	18 CTTGTGCGCGCGGCTTCTGTGTGATGGCGCGCTGACGATGAGGAGCTGCGTGGCGGCGCA	77		
Qy	121 ACTGACGATGAGCGAGATGACGAGCTCCG	150		
Dd	78 GCTGTCGATCACGACACTTCCAGGTGG	107		
RESULT 34				
LOCUS	CQ424819	170 bp	DNA	linear PAT 28-JAN-2004
DEFINITION	Sequence 9853 from Patent WO0151628.			
ACCESSION	CQ424819			
VERSION	CQ424819.1 GI:41377048			
KEYWORDS	.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	Lillie,J., Xu,Y., Wang,Y. and Steinmann,K.			
TITLE	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer Patent: WO 0151628-A 9853 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)			
JOURNAL	Location/Qualifiers			
FEATURES	1..170			
Source	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"			

Qy	5	CGAGCTGTCATCTCGCTCATCTGCATGTCGCGCGCGGAGCTGTCATCTCGCTCATC	64
Db	107	CCGACCTGGAAAGTGTCCGATGATTCAGCAGGCTGCGCGCGAGCGAGCCCATCTCATCGC	48
Qy	65	GTCAGTCGCGGCGCGCGCATCTGCAGCATG	94
Db	47	GCGCCATCGACACGAGACCGGCGCAGCAAG	18
RESULT.35			
LOCUS	CQ416921	189 bp	DNA
DEFINITION	Sequence 1955 from Patent WO0151628.	linear	PAT 28-JAN-2004
ACCESSION	CQ416921		
VERSION	CQ416921.1	GI:41369150	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1. Lillie,J., Xu,Y., Wang,Y. and Steilmann,K.		
TITLE	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer		
JOURNAL	Patent: WO 0151628-A 1955 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1. 189		
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	/mol_type="unassigned DNA"		
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Best Local Similarity	55.6%;	Pred. No. 1.8e+05;	
Matches	50;	Conservative	0; Mismatches 40; Indels 0; Gaps 0;
Qy	61	CATGTCGAGTCGCGCGCGCGCGCATCTGCAGCATGAGCAGATGACCAAGCTTCGCGCGCG	120
Db	33	CTTCGTGGCGCGCGTTCGTGTCATGTGCGCGCGCGCGCATGAGTGCGGTGTCGCGCGCGCA	92
Qy	121	ACTGCAGCATGAGCGCAGATGACCAAGCTTCG	150
Db	93	GCTCGTCATCACCGACACTTCACAGTTCGG	122
RESULT.36			
LOCUS	CQ416921/c	189 bp	DNA
DEFINITION	Sequence 1955 from Patent WO0151628.	linear	PAT 28-JAN-2004
ACCESSION	CQ416921		
VERSION	CQ416921.1	GI:41369150	
KEYWORDS			
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS	1. Lillie,J., Xu,Y., Wang,Y. and Steilmann,K.		
TITLE	Novel genes, compositions, kits, and methods for identification, assessment, prevention, and therapy of breast cancer		
JOURNAL	Patent: WO 0151628-A 1955 19-JUL-2001; Millennium Pharmaceuticals, Inc. (US)		
FEATURES	Location/Qualifiers		
source	1. 189		
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ORIGIN /db_xref="taxon:32644"

Query Match 16.6%; Score 26; DB 6; Length 189;
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Matches 50; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

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DB 122 CCGACCTGGAAGTCTCGGTATGACGAGCTGCCGCCGAGCGCAGCCCCATCTGTCAGC 63

QY 65 GTCGAGTCGGCGCGCCCGCATCGACGATG 94
DB 62 GCCCATCGACGAGACCGCGCGCAGCAG 33

RESULT 37
A58814 183 bp DNA linear PAT 06-MAR-1998
LOCUS
DEFINITION Sequence 3 from Patent WO9638587.
ACCESSION A58814
VERSION A58814.1 GI:3714345
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Chrzavetz, E. E. and Aufreere, R.
TITLE METHOD FOR DETECTING HEAT-RESISTANT MICRO-ORGANISMS CAPABLE OF
JOURNAL CONTAMINATING CERTAIN FOOD PRODUCTS
COMMENT Patent: WO 9638587-A 3 05-DEC-1996;
FEATURES ULTRA PROBE NUTRITION IND REC (FR)
Other publication FR 2734844 961206.
Location/Qualifiers
1. 183
/organism="unidentified"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 16.6%; Score 25.6; DB 6; Length 183;
Best Local Similarity 59.7%; Pred. No. 2.2e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 64 CGTCGAGTCGGCGCGCCCGCATCTGACGATGAGCGAGATGACCAAGTCCGCGCCGCACT 123
DB 67 CGCGGTTTCAGCGCGCCCGCGGAGGCTCTCGCGCCCGCGCGCCCGCCGCAAGACC 126

QY 124 CGACGATGAGCG 135
DB 127 CCAACATGAACG 138

RESULT 38
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LOCUS
DEFINITION Sequence 3 from Patent WO9638587.
ACCESSION A58814
VERSION A58814.1 GI:3714345
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Chrzavetz, E. E. and Aufreere, R.
TITLE METHOD FOR DETECTING HEAT-RESISTANT MICRO-ORGANISMS CAPABLE OF
JOURNAL CONTAMINATING CERTAIN FOOD PRODUCTS
COMMENT Patent: WO 9638587-A 3 05-DEC-1996;
FEATURES ULTRA PROBE NUTRITION IND REC (FR)
Other publication FR 2734844 961206.
Location/Qualifiers
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Query Match 16.6%; Score 25.6; DB 6; Length 183;
Best Local Similarity 59.7%; Pred. No. 2.2e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 20 CGCTCATCTGTCAGTCCGCGCGCGGAGCTGTCATCTGCTCATCTGTCAGTCCGCGCC 79
DB 138 CGTTTCATGTTGGGGTCTTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTCCCGCGCGCC 79

QY 80 GCCGACTCGACG 91
DB 78 GTCGAACGCGCG 67

RESULT 39
AR110714 183 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 3 from patent US 6117636.
ACCESSION AR110714
VERSION AR110714.1 GI:12827528
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 183)
AUTHORS Chrzavetz nee Taddel, E. and Aufreere, R.
TITLE Method for detecting heat-resistant micro-organisms capable of
JOURNAL contaminating certain food products
FEATURES Patent: US 6117636-A 3 12-SEP-2000;
Location/Qualifiers
1. 183
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/mol_type="unassigned DNA"

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Best Local Similarity 59.7%; Pred. No. 2.2e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 64 CGTCGAGTCGGCGCGCCCGCATCTGACGATGAGCGAGATGACCAAGTCCGCGCCGCACT 123
DB 67 CGCGGTTTCAGCGCGCCCGCGGAGGCTCTCGCGCCCGCGCGCCCGCCGCAAGACC 126

QY 124 CGACGATGAGCG 135
DB 127 CCAACATGAACG 138

RESULT 40
AR110714/c 183 bp DNA linear PAT 14-FEB-2001
LOCUS
DEFINITION Sequence 3 from patent US 6117636.
ACCESSION AR110714
VERSION AR110714.1 GI:12827528
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 183)
AUTHORS Chrzavetz nee Taddel, E. and Aufreere, R.
TITLE Method for detecting heat-resistant micro-organisms capable of
JOURNAL contaminating certain food products
FEATURES Patent: US 6117636-A 3 12-SEP-2000;
Location/Qualifiers
1. 183
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Best Local Similarity 59.7%; Pred. No. 2.2e+05;
Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Matches 43; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 20 CGCTCATGCTGAGTCCGCGCGGAGCTGATCTGCTCATGCTGAGTCCGCGGCC 79
Db 138 CGTTCATGTTGGGCTTTCGGCGCGGCGCGCGCGCGGAGGCTCCCGCGCGCC 79

Qy 80 GCCGACTCGAGC 91
Db 78 CTCGAACGCGC 67

RESULT 41
ALUJ3657 105 bp DNA linear VRT 15-JUN-2001
LOCUS Apterionotus leptorhynchus 28S ribosomal RNA gene, partial sequence.
DEFINITION U33657
ACCESSION U33657.1 GI:2443919
VERSION
KEYWORDS
SOURCE Apterionotus leptorhynchus
ORGANISM Apterionotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apterionotidae; Apterionotus.
REFERENCE 1 (bases 1 to 105)
AUTHORS Dimmick,W.W. and Larson,A.
TITLE A molecular and morphological perspective on the phylogenetic relationships of the otophysean fishes
JOURNAL Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)
MEDLINE 96426866
PUBMED 8812312
REFERENCE 2 (bases 1 to 105)
AUTHORS Dimmick,W.W. and Larson,A.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1995) University of Kansas, Dyché Hall, Jayhawk Boulevard, Lawrence, KS 66045, USA
LOCATION/Qualifiers
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/organism="Apterionotus leptorhynchus"
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/issue_type="muscle"
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Query Match 16.5%; Score 25.4; DB 5; Length 105;
Best Local Similarity 60.3%; Pred. No. 2.7e+05;
Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 20 CGCTCATGCTGAGTCCGCGCGGAGCTGATCTGCTCATGCTGAGTCCGCGGCC 79
Db 37 CGCGCCGCGCGCGGAGCTGATCTGCTCATGCTGAGTCCGCGGCC 96

Qy 80 GCCGACTC 87
Db 97 GCGTACCC 104

RESULT 42
ALUJ3657 105 bp DNA linear VRT 15-JUN-2001
LOCUS Apterionotus leptorhynchus 28S ribosomal RNA gene, partial sequence.
DEFINITION U33657
ACCESSION U33657.1 GI:2443919
VERSION
KEYWORDS
SOURCE Apterionotus leptorhynchus
ORGANISM Apterionotus leptorhynchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Gymnotiformes; Apterionotidae; Apterionotus.
REFERENCE 1 (bases 1 to 105)
AUTHORS Dimmick,W.W. and Larson,A.

TITLE A molecular and morphological perspective on the phylogenetic relationships of the otophysean fishes
JOURNAL Mol. Phylogenet. Evol. 6 (1), 120-133 (1996)
MEDLINE 96426866
PUBMED 8812312
REFERENCE 2 (bases 1 to 105)
AUTHORS Dimmick,W.W. and Larson,A.
TITLE Direct Submission
JOURNAL Submitted (10-AUG-1995) University of Kansas, Dyché Hall, Jayhawk Boulevard, Lawrence, KS 66045, USA
LOCATION/Qualifiers
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/organism="Apterionotus leptorhynchus"
/mol_type="genomic DNA"
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/issue_type="muscle"
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/product="28S ribosomal RNA"

ORIGIN
Query Match 16.5%; Score 25.4; DB 5; Length 105;
Best Local Similarity 60.3%; Pred. No. 2.7e+05;
Matches 41; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

Qy 68 GAGTCGCGCGCGCGGAGCTGAGTCCGCGCGGAGCTGAGTCCGCGGCC 127
Db 104 GAGTCGCGCGCGGAGCTGAGTCCGCGCGGAGCTGAGTCCGCGGCC 45

Qy 128 GATGAGCG 135
Db 44 GCGCGCGC 37

RESULT 43
ABI64173 165 bp DNA linear BCT 10-MAR-2004
LOCUS ABI64173
DEFINITION Uncultured bacterium nirs gene for nitrite reductase, partial cds,
ACCESSION ABI64173
VERSION ABI64173.1 GI:45330786
KEYWORDS
SOURCE uncultured bacterium
ORGANISM uncultured bacterium
Bacteria; environmental samples.
REFERENCE 1
AUTHORS Shoji,T.
TITLE Microbial communities of an enhanced biological phosphorus removal process using oxygen, nitrate and nitrite as electron acceptors
JOURNAL Unpublished
AUTHORS Shoji,T.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2004) Tadaishi Shoji, The University of Tokyo, Department of Urban Engineering, 7-3-1, Hongo, Bunkyo, Tokyo 113-8656, Japan (E-mail:shoji@env.t.u-tokyo.ac.jp, Tel:81-3-5841-7784, Fax:81-3-5841-8538)
LOCATION/Qualifiers
FEATURES
source 1..165
/organism="uncultured bacterium"
/mol_type="genomic DNA"
/isolate="DGSB band f2r5-sa"
/isolation_source="activated sludge from lab-scale SBR fed with wastewater"
/db_xref="taxon:77133"
/environmental_sample
/country="Japan:Tokyo"
/note="PCR products amplified by primers nirs2fGC and nirs3R were analyzed by DGSB"
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GenCore version 5.1.6
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Title: US-09-887-194A-13

Perfect score: 154
Sequence: 1 cggcgcgagctgtgcatctc.....gagatgaccagctccgagcgcg 154

Scoring table: IDENTITY_NUC
Gap 10.0 , Gape 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

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2: gb_esc2: *
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8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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29	35.8	23.2	367	5	BQ767987
30	35.8	23.2	367	5	BQ767987
31	35.6	23.1	397	9	CE011375
32	35.6	23.1	397	9	CE011375
33	35.6	23.1	624	6	CB682412
34	35.6	23.1	624	6	CB682412
35	35.6	23.1	677	6	CA198784
36	35.6	23.1	677	6	CA198784
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38	35.4	23.0	590	1	AI139069
39	35.4	23.0	704	6	CA227997
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43	35	22.7	571	5	B0805125
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48	34.8	22.6	497	1	AL829848
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81	34.2	22.2	600	6	CB689196
82	34.2	22.2	600	6	CB689196
83	34.2	22.2	606	5	B0939339
84	34.2	22.2	606	5	B0939339
85	34.2	22.2	645	6	CB688201
86	34.2	22.2	645	6	CB688201
87	34.2	22.2	647	4	B1960178
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BF462402	UI-M-CGDP	
BF466956	UI-M-CGDP	
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CL950005	OsIRUA001	
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B0939339	HM05A17r	
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CB688201	CEST-10-H	
CB688201	CEST-10-H	
B1960178	HVSMEM002	
B1960178	HVSMEM002	
AU078265	AU078265	
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BF622282	HVSMEM000	
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BM816829	HCO3D11_T	
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ALIGNMENTS

RESULT 1					
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LOCUS	BZ566906	512 bp	DNA	linear	GSS 17-DEC-2002
DEFINITION	pac62-164 6657.x1 pac62-164 <i>Pseudomonas aeruginosa</i> genomic clone				
	pac62-164_6657, genomic survey sequence.				

ACCESSION	B2566906	
VERSION	B2566906.1	GI:27197291
KEYWORDS	GSS.	
SOURCE	<i>Pseudomonas aeruginosa</i>	
ORGANISM	<i>Pseudomonas aeruginosa</i>	

REFERENCE 1 (bases 1 to 512)

TITLE	Whole-Genome-Sequence variation among multiple isolates of
JOURNAL	<i>Pseudomonas aeruginosa</i> library
COMMENT	<i>J. Bacteriol.</i> (2002) In press
	Contact: Chris K. Raymond

University of Washington
Box 352115, Seattle, WA 98105-2145, USA
Tel.: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

```

FEATURES
    source
        location/Qualifiers
            1..512
            /organism="Pseudomonas aeruginosa"
            /mol_type="genomic DNA"
            /strain="2-164"
            /db_xref="taxon:287"
            /clone="pac82-164.6657"
            /clone_1b="pac82_164"
            /note="clinical isolate 2-164 whole genomic shotgun
            library."

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Query Match	Score	DB	Length
24.8%	38.2	8	512

Best Local Similarity 61.6%; Pred. NO. 12;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

0y | GCGGCGAGCTGGTCATCTGGCTATCGTCAAGTGCGGCGGGCGCCGACTCAGCATGATGAG 96
37 |
Db | 360 GCTGTGATGATCGTCAACCCGCACCTGGTCCAGCCGCTGGCGGCCAAGCGCACAGATTGCC 419

420 GGACCTGCCCGCGGAGGCGCTGCGGCACTACGATCCGGG 458

RESULT 2			
B2566906/c			
LOCUS	B2566906	512 bp	DNA
DEFINITION	pac62-164.6657.x1 pac62-164 Pseudomonas aeruginosa genomic clone		
	pac62-164.6657, genomic survey sequence.		

KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
GS.		<i>Pseudomonas aeruginosa</i>		
66-6750-1	612/15/221	<i>Pseudomonas aeruginosa</i>		
		Bacteria, Proteobacteria, Gammaproteobacteria, Pseudomonadales		
		Pseudomonadaceae, Pseudomonas.		
		(bases 1 to 512)		
		Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.		

TITLE	Burns, J.L., Kaul, R. and Olsen, M.V. Whole-Genome-Sequence variation among multiple isolates of
JOURNAL	<i>Pseudomonas aeruginosa</i> library
COMMENT	J. Bacteriol. (2002) In press Contact: Chris K. Raymond

University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Tel: 2066857244
Fax: 2066857244
Email: craymond@u.washington.edu
Class: Shotgun.

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FEATURES
source
location/Qualifiers
1..512
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="2-164"
/db_xref="taxon:287"
/clone="pacs2-164_6657"
/clone_1fb="pacs2-164"
/notes="clinical isolate 2-164 Whole genomic shotgun
library."

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ORIGIN

Query Match	24.8%	Score 38.2;	DB 8;	Length 512;
Best Local Similarity	61.6%;	Pred. No. 12;		
Matches 61; Conservative	0;	Mismatches 38;	Indels 0;	Gaps 0

Qy 20 CGTCATCGTCGAGTCGGCGCCGGAGCTGGTCATTCGCTCATCGTCGAGTCGGCGCC 79
Db 458 CCCGATCGTAGTGC CGCAGGCCCTCGCCGGCAGGTC CGGCACTGTGCTCGGCGCC 399

QY 80 GCCGACTGCAGTAgCGGATGACCAgCTCCGGCCG 118
Db 398 AGCGGCTGACCAgGTGCGGGGTGACGATCATCAGCAGC 360

RESULT 3				
CD931316				
LOCUS	CD931316	513 bp	mRNA	linear
DEFINITION	GR45.114C04F010419	GR45	Triticum aestivum	CDNA clone GR45114C04,

ACCESSION	CD931316	
VERSION	CD931316.1	GI:32779080
KEYWORDS	EST.	

SOURCE

ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.
1 (bases 1 to 513)
Genoplante.

REFERENCE
AUTHORS

TITLE	Genoplane, a major partnership french program in plant genomics
JOURNAL	Unpublished (2003)
COMMENT	Contact: Genoplane

Genoplante
93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplante' (<http://www.genoplante.com>
and <http://genoplante-info.infobogen.fr>).

FEATURES	Location/Qualifiers
source	1. .513

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/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="rectal"
/db_xref="taxon:4565"
/clone="GR4511C04"
/tissue_type="grain (45 degrees per day after
pollination)"
/clone_1ib="GR45"

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ORIGIN

Query Match 24.8%; Score 38.2; DB 6; Length 513;
 Best Local Similarity 53.7%; Pred. No. 12;
 Matches 79; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 8 AGCTGTCATCTCGCTCATCTGTCAGTGGCGCGGAGCTGTCATCTCGCTCATCTGTC 67
 DB 138 AACGAGGCGTCCAAACACTCTCTCCCGCCCAAGCTCGCCCTCGACCTGTGCTCACCGTC 197

QY 68 GAGTCGGCGCGCGCGGCTGACGATGAGCGAGATGACCACTCGCGCGCGGCTGAC 127
 DB 198 ACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 257

QY 128 GATGAGCGAGATGACGAGCTCGCGCGCG 154
 DB 258 GCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 284

RESULT 4
 CD931316/c 513 bp mRNA linear EST 15-JUL-2003
 LOCUS GR45.114C04F010419 GR45 Triticum aestivum cDNA clone GR45114C04,
 DEFINITION mRNA sequence.
 ACCESSION CD931316
 VERSION CD931316.1 GI:32779080
 KEYWORDS EST.
 SOURCE Triticum aestivum (bread wheat)
 ORGANISM Triticum aestivum

REFERENCE
 AUTHORS Genoplane.
 TITLE Genoplane, a major partnership french program in plant genomics
 JOURNAL Unpublished (2003)
 COMMENT Contact: Genoplane
 Genoplane
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00
 Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme 'Genoplane' (<http://www.genoplane.com>
 and <http://genoplane-info.infobiogen.fr>).
 Location/Qualifiers
 1..513
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /culturivar="recital"
 /db_xref="taxon:4565"
 /clone="GR45114C04"
 /tissue_type="grain (45 degrees per day after
 pollination)"
 /clone_id="GR45"

ORIGIN

Query Match 24.8%; Score 38.2; DB 6; Length 513;
 Best Local Similarity 54.7%; Pred. No. 12;
 Matches 76; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 9 GCTGTCATCTCGCTCATCTGTCAGTGGCGCGGAGCTGTCATCTCGCTCATCTGTC 68
 DB 276 GCTGCGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCTG 217

QY 69 AGTCGCGCGCGCGCGGACTCGACGATGAGCGAGATGACGAGTCCGCGCGCGGACTCGACG 128
 DB 216 TGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 157

QY 129 ATGAGCGAGATGACGAGCT 147
 DB 156 AGGTGTTGAGCGCTCGTT 138

RESULT 5

CL981398 1878 bp DNA linear GSS 21-SEP-2004
 LOCUS OaIFCC045611 Oryza sativa Express Library Oryza sativa (indica
 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL981398
 VERSION CL981398.1 GI:52417290
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euhartoidae; Oryzaceae; Oryza.
 1 (bases 1 to 1878)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis
 Unpublished (2004)
 Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.
 Location/Qualifiers
 1..1878
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_id="Oryza sativa Expressed Library"
 /note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 24.0%; Score 37; DB 9; Length 1878;
 Best Local Similarity 53.0%; Pred. No. 23;
 Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTGTCATCTGTCATCTGTCAGTGGCGCGGAGCTGTCATCTGTC 60
 DB 837 GCTCCGAGCGGCGCTCTCTCTGCGCGCGCGCTGCGCTGCTGCTGCGCCACTGCT 896

QY 61 CATCTGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 DB 897 GCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 956

QY 121 ACTCGAGATGAGCGAGATGACGAGCTCC 149
 DB 957 CTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 985

RESULT 6

CL981398/c 1878 bp DNA linear GSS 21-SEP-2004
 LOCUS OaIFCC045611 Oryza sativa Express Library Oryza sativa (indica
 DEFINITION cultivar-group) genomic, genomic survey sequence.
 ACCESSION CL981398
 VERSION CL981398.1 GI:52417290
 KEYWORDS GSS.
 SOURCE Oryza sativa (indica cultivar-group)
 ORGANISM Oryza sativa (indica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euhartoidae; Oryzaceae; Oryza.
 1 (bases 1 to 1878)
 Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
 Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
 Wong, G.K.S., Deng, X.W. and Wang, J.
 An analysis of transcriptional regulation of the rice genome and
 its comparison to Arabidopsis

JOURNAL Unpublished (2004)
 COMMENT Contact: Chen Chen
 Department of Bioinformatic
 Beijing Institute of Genomics
 Chinese Academy of Sciences, Beijing 101300, China
 Tel: 86-10-80481559
 Fax: 86-10-80488676
 Email: chenchen@genomics.org.cn
 Rice genomic sequence.
 Class: exon-trapped.

FEATURES
 source location/Qualifiers
 1..1878
 /organism="Oryza sativa (indica cultivar-group)"
 /mol_type="genomic DNA"
 /db_xref="taxon:39946"
 /clone_lib="Oryza sativa Express library"
 /note="Oryza sativa exon trapped genomic sequences"

ORIGIN

Query Match 24.0%; Score 37; DB 9; Length 1878;
 Best Local Similarity 53.0%; Pred. No. 23;
 Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Oy 6 GGAGCTGCTATCTCGCTCATGCTCGAGTCCGGCGCGAGCTGCTATCTCGCTCATCG 65
 |||||
 Db 985 GGCGCTGCACGCTCGCTCCCGGCTGCGAGACGCGGGCGAGAGCAGCTCTCGAGGGACG 926
 |||||

Oy 6 TCGAGTCCGGCGCGCGGCTCGACATCGACGATGACGATACGACGCTCCGGCGCGGACATCG 125
 |||||
 Db 925 GCAGGGCCATGCGCCCGCGCGCGGCGAGACGACGATGCGCCGACGACGAGCGACGCG 866
 |||||

Oy 126 ACGATGACGAGATGACGACGCTCCGGCGG 154
 |||||
 Db 865 CCGCGCAGAGAGAGAGCCGCTCGGAGCG 837
 |||||

RESULT 7
 BF945949 175 bp mRNA linear EST 22-JAN-2001
 LOCUS CMO-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF945949
 ACCESSION BF945949.1 GI:12363224
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 175)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,U.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800

TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 MEDLINE Ludwig Institute for Cancer Research
 PUBMED Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NN1155-
 271000-628-a09&t3=2000-10-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 13

FEATURES High quality sequence stop: 175.
 source location/Qualifiers
 1..175
 /organism="Homo sapiens"
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 /dev_stage="Adult"
 /clone_lib="NN1155"
 /note="Organ: nervous normal; Vector: puc18; Site 1: Sma1;
 Site 2: Sma1; A mini-library was made by cloning products
 derived from ORSTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN

Query Match 23.8%; Score 36.6; DB 4; Length 175;
 Best Local Similarity 65.1%; Pred. No. 32;
 Matches 54; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Oy 70 GTCCGCGCGCGCGATCTGCATGACGAGATGACGATCGCGCGCGGACTGACGA 129
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 Db 7 GTCGTGCGCGTGGCTGGCTGGTGGAGGAGAACACCACTCGCGCGGTAGCTGGATGG 66
 |||||

Oy 130 TGAAGAGATGACGACGCTCGGC 152
 |||||
 Db 67 TGAAGAGATGACCACTCGGC 89
 |||||

RESULT 8
 BF945949 175 bp mRNA linear EST 22-JAN-2001
 LOCUS CMO-NN1155-271000-628-a09 NN1155 Homo sapiens cDNA, mRNA sequence.
 DEFINITION BF945949
 ACCESSION BF945949.1 GI:12363224
 VERSION
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 175)
 Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
 Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
 Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,U.F., de Souza,S.J. and
 Simpson,A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 10737800

TITLE Contact: Simpson A.J.G.
 JOURNAL Laboratory of Cancer Genetics
 MEDLINE Ludwig Institute for Cancer Research
 PUBMED Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CMO&t2=CMO-NN1155-
 271000-628-a09&t3=2000-10-27&t4=1)
 Seq primer: puc 18 forward
 High quality sequence start: 13
 High quality sequence stop: 175.
 Location/Qualifiers
 1..175
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"

/dev stage="Adult"
/clone_1ib="NN155"
/note="Organ: nervous normal; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 23.8%; Score 36.6; DB 4; Length 175;
Best Local Similarity 65.1%; Pred. No. 32;
Matches 54; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 3 GCCGAGCTGTCATCTGCTCATGTCAGTCGCGCGGAGCTGTCATCTGCTCA 62
Db 89 GCCGAGCTGTCATCTGCTCATGTCAGTCGCGCGGAGCTGTCATCTGCTCA 30

Qy 63 TCGTCAGTCGCGCGCGGAGCTGTCATCTGCTCATGTCAGTCGCGCGGAGCTGTCATCTGCTCA 85
Db 29 CCACCCAGCTTACCGCCACAGAC 7

RESULT 9 514 bp mRNA linear EST 14-JUL-2003
CD895591
LOCUS G174.100E07F010705 G174 Triticum aestivum cDNA clone G174100E07,
DEFINITION mRNA sequence.
ACCESSION CD895591
VERSION CD895591.1 GI:32668349
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 514)
AUTHORS Genoplane, a major partnership french program in plant genomics
TITLE Genoplane, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplane
Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>
and <http://genoplane-info.infobiogen.fr>).
Location/Qualifiers
1..514
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultiyar="recital"
/db_xref="taxon:4565"
/clone="G174100E07"
/tissue_type="grain (174 degrees per day after
pollination)"
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ORIGIN
Query Match 23.8%; Score 36.6; DB 6; Length 514;
Best Local Similarity 53.1%; Pred. No. 31;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 8 AGTGTGATCTCTCTATCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 67
Db 314 AACGAGGCTCCAACTCTCTCTGCGCGGAGCTGTCATCTGCTCATGCTC 373

Qy 68 GAGTCGCGCGCGGAGCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 127
Db 374 ACCGCGCGCGCGGAGCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 433

ORIGIN

Query Match 23.8%; Score 36.6; DB 6; Length 514;
Best Local Similarity 53.1%; Pred. No. 31;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 8 AGTGTGATCTCTCTATCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 67
Db 314 AACGAGGCTCCAACTCTCTCTGCGCGGAGCTGTCATCTGCTCATGCTC 373

Qy 68 GAGTCGCGCGCGGAGCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 127
Db 374 ACCGCGCGCGCGGAGCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 433

Qy 128 GATGAGCGAGTACACAGCTCCGCGG 154
Db 434 GCGGAGCGCGCGGAGCTCCGAGCGG 460

RESULT 10 514 bp mRNA linear EST 14-JUL-2003
CD895591
LOCUS G174.100E07F010705 G174 Triticum aestivum cDNA clone G174100E07,
DEFINITION mRNA sequence.
ACCESSION CD895591
VERSION CD895591.1 GI:32668349
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum

REFERENCE 1 (bases 1 to 514)
AUTHORS Genoplane, a major partnership french program in plant genomics
TITLE Genoplane, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplane
Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>
and <http://genoplane-info.infobiogen.fr>).
Location/Qualifiers
1..514
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultiyar="recital"
/db_xref="taxon:4565"
/clone="G174100E07"
/tissue_type="grain (174 degrees per day after
pollination)"
/clone_1ib="G174"

FEATURES

ORIGIN
Query Match 23.8%; Score 36.6; DB 6; Length 514;
Best Local Similarity 54.0%; Pred. No. 31;
Matches 75; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 9 GCTGTGATCTCTCTATCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 68
Db 452 GCTGTGATCTCTCTATCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 393

Qy 69 AGTGTGATCTCTCTATCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 128
Db 392 TGGGCGCGCGGAGCTGTCAGTCGCGCGGAGCTGTCATCTGCTCATGCTC 333

Qy 129 ATGAGCGAGTACACAGCT 147
Db 332 AGTGTGAGCTCTGTT 314

ORIGIN

RESULT 11 653 bp DNA linear GSS 16-DEC-2002
B2509933
LOCUS BOMQPI4TF BO_2_3_KB Brassica oleracea genomic clone BOMQPI4,
DEFINITION genomic survey sequence.
ACCESSION B2509933
VERSION B2509933.1 GI:27033989
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 653)
AUTHORS Genoplane, a major partnership french program in plant genomics
TITLE Genoplane, a major partnership french program in plant genomics
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplane
Genoplane
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplane' (<http://www.genoplane.com>
and <http://genoplane-info.infobiogen.fr>).
Location/Qualifiers
1..653
/organism="Brassica oleracea"
/mol_type="DNA"
/cultiyar="recital"
/db_xref="taxon:4565"
/clone="BOMQPI4TF"
/tissue_type="grain (174 degrees per day after
pollination)"
/clone_1ib="BOMQPI4TF"

AUTHORS Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished (2001)
 COMMENT Other_GSSs: BOMQF14TR
 Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208

Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TF
 Class: sheared ends.

FEATURES

source Location/Qualifiers

1..653
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOMQF14"
 /clone_lib="BO_2_3 KB"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score:36.4; DB 8; Length 653;
 Best Local Similarity 55.6%; Pred. No. 34;
 Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 18 CTCGCTATCGTCGAGTGGCGGCGGAGCTGTCATCTCGCTCATCGTCAGTGGCGG 77
 DB 359 CTCGCCATGGCGCGGAGTGACCTCTGCGCGGCTCTCTCCGCCATGGCGGAGTGACCA 418
 QY 78 CCGCCGACTCGACGATGACGAGATGACAGCTCGCGCGCGAGCTGACGATGAGGAG 137
 DB 419 TGGGGAGAGTACCATGGGCGAGGAGCTCGGTCGCGGCTTCTCTCCTGAGGCGGAG 478
 QY 138 ATGACC 143
 DB 479 GTGATC 484

RESULT 12
 BZ509933/c 653 bp DNA linear GSS 16-DEC-2002
 LOCUS BOMQF14TF BO_2_3 KB Brassica oleracea genomic clone BOMQF14,
 DEFINITION genomic survey sequence.
 ACCESSION BZ509933
 VERSION BZ509933.1 GI:27033989
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 653)
 AUTHOR Town,C.D., Van Aken,S., Uteerback,T., Koo,H. and Fraser,C.M.
 TITLE Whole genome shotgun sequencing of Brassica oleracea
 JOURNAL Unpublished (2001)
 COMMENT Other_GSSs: BOMQF14TR
 Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

FEATURES

source Location/Qualifiers

1..653
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"

/strain="TO1000DH3"
 /db_xref="taxon:3712"
 /clone="BOMQF14"
 /clone_lib="BO_2_3 KB"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 653;
 Best Local Similarity 55.6%; Pred. No. 34;
 Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 12 GGTATCTCGCTATCGTCGAGTGGCGGCGGAGCTGTCATCTCGCTCATCGTCA 71
 DB 484 GATCACTCGCCCTGAGCGAGAGACCCGACCGAGTCACTCGCCATGTCACCT 425
 QY 72 CGGCGCGCGGACTCGACGATGACGAGATGACCAAGCTCGGCGCGGACTGACGATG 131
 DB 424 CGCCATGTGTCACCTGCGCCATGGGCGAGACGACCGCGGAGAGTCACTCGCCCATG 365
 QY 132 AGCGAG 137
 DB 364 GCGGAG 359

RESULT 13
 BH925906 711 bp DNA linear GSS 01-OCT-2002
 LOCUS odg84c07.g1 B.oleracea002 Brassica oleracea genomic, genomic survey
 DEFINITION sequence.
 ACCESSION BH925906
 VERSION BH925906.1 GI:23405972
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 711)

AUTHORS Delehaunty,K., Fewell,G., Fulton,L., McComble,W.R., Miner,T.,
 Nash,W., Rabinowicz,P.D. and Wilson,R.K.
 TITLE Whole genome shotgun reads from Brassica oleracea
 JOURNAL Unpublished (2002)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu

Plate: odg84 row: c column: 07
 Seq primer: -28RPpOT reverse

Class: shotgun

High quality sequence start: 16
 High quality sequence stop: 551.

FEATURES

source Location/Qualifiers

1..711
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_lib="B.oleracea002"
 /note="Vector: pOTw13; Whole genome shotgun library from
 flowering buds. DNA was purified from a crude nuclear
 prep using Brassica oleracea TO1000DH3 buds provided by
 Thomas Osborn at the University of Wisconsin.
 DNA was provided by Pablo Rabinowicz (CSHL) and the
 shotgun library prepared at Washington University Genome
 Sequencing Center."

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 711;
 Best Local Similarity 55.6%; Pred. No. 34;
 Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 18 CTCGCTATCGTCGAGTGGCGGCGGAGCTGTCATCTCGCTCATCGTCAGTGGCGG 77

Db 405 CTCGCCCATGGGCGAGGTGATGACTCTGCGCGGGCTCTCCGCCCATGGGCGAGGTGACCA 464

Qy 78 CCGCGCACTGCGACGATGAGGAGATGACCACTCCGCGCCCGCACTGACATGAGGAG 137

Db 465 TGGCGGAGGTGACCATGGGCGAGGTGACTCGTGGGGTCTTCTCGCTGCGAGGCGGAG 524

Qy 138 ATGACC 143

Db 525 GTGATC 530

RESULT 14
BH925906/c

LOCUS 711 bp DNA linear GSS 01-OCT-2002

DEFINITION odc84c07.g1 B.oleracea002 Brassica oleracea genomic, genomic survey sequence.

ACCESSION BH925906

VERSION BH925906.1 GI:23405972

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 711)

Delehanthy, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: submision@wustl.edu

Plate: odc84 row: c column: 07

Seq primer: -28RPOT reverse

Class: shotgun

High quality sequence start: 16

High quality sequence stop: 551.

Location/Qualifiers

1..711

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/db_xref="taxon:3712"

/clone.lib="B.oleracea002"

/note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea T0100DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 711;

Best Local Similarity 55.6%; Pred. No. 34;

Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 12 GGTGATCTGCTATCTGATGAGTGGCGGCGGAGCTGTCATCTGCTATCTGAGT 71

Db 530 GATCACTTCGCGCCCTGAGCGAGGAAGACCCGACCGAGTCACTCGCCCATGTGTCACCT 471

Qy 72 CGGCGCGCGCGCATGACGATGAGGAGACGACAGTCCGCGCGCGCATGACGATG 131

Db 470 CGCCCATGTGATCTCGCCCATGGGCGAGGACGACGACCGCGGAGGATCACTCGCCCATG 411

Qy 132 AGCGAG 137

Db 410 GCGGAG 405

RESULT 15
B2427562

LOCUS 818 bp DNA linear GSS 13-DEC-2002

DEFINITION BONUT45TR BO_1.6.2 KB tot Brassica oleracea genomic clone BONUT45, genomic survey sequence.

ACCESSION B2427562

VERSION B2427562.1 GI:26669268

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 818)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other GSSs: BONUT45TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1..818

/organism="Brassica oleracea"

/mol_type="genomic DNA"

/strain="T0100DH3"

/db_xref="taxon:3712"

/clone.lib="BONUT45"

/note="Vector: pHO51; Site 1: BstXI; 1.6-2 kb sheared total DNA inserted into pHO51 using BstXI linkers"

ORIGIN

Query Match 23.6%; Score 36.4; DB 8; Length 818;

Best Local Similarity 55.6%; Pred. No. 34;

Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

Qy 12 GGTGATCTGCTATCTGATGAGTGGCGGCGGAGCTGTCATCTGCTATCTGAGT 71

Db 291 GATCACTTCGCGCCCTGAGCGAGGAAGACCCGACCGAGTCACTCGCCCATGTGTCACCT 350

Qy 72 CGGCGCGCGCGCATGACGATGAGGAGACGACAGTCCGCGCGCGCATGACGATG 131

Db 351 CGCCCATGTGATCTCGCCCATGGGCGAGGACGACGACCGCGGAGGATCACTCGCCCATG 410

Qy 132 AGCGAG 137

Db 411 GCGGAG 416

RESULT 16
B2427562

LOCUS 818 bp DNA linear GSS 13-DEC-2002

DEFINITION BONUT45TR BO_1.6.2 KB tot Brassica oleracea genomic clone BONUT45, genomic survey sequence.

ACCESSION B2427562

VERSION B2427562.1 GI:26669268

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 818)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Whole genome shotgun sequencing of Brassica oleracea

Unpublished (2001)

Other GSSs: BONUT45TF

Contact: Chris Town

TIGR

QY	123	TCGACG	128
Db	349	GCGCCG	344

RESULT 19
CNS030BV
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone 041B18 of library G from Tetraodon nigroviridis, genomic survey sequence.
AL253156.1 GI:7974168
VERSION
KEYWORDS
GSS: genome survey sequence.
SOURCE
ORGANISM
Tetraodon nigroviridis
Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE
AUTHORS
1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL
MEDLINE
20296633
PUBMED
10835645
REFERENCE
AUTHORS
2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costraz,C., Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
JOURNAL
MEDLINE
20359837
PUBMED
10899143
COMMENT
TITLE
Genoscope.
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.
FEATURES
source
location/Qualifiers
1..627
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="041B18"
/clone_lib="G"
/note="Genoscope sequence ID : COBG041DA09LP1-end : T7"
ORIGIN
Query Match 23.5%; Score 36.2; DB 9; Length 627;
Best Local Similarity 65.4%; Pred. No. 38;
Matches 53; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
QY 55 CTCGCTCATCGTCGAGTGGGCGCGCGACTCGACGATGAGCGAGTACCACTCCGG 114
Db 342 CTCGCTCATGCTCTGTCGCGCGAGAGAGTCTCGGACGCGCGAGACACAGAGCGG 401
QY 115 CCGCGGACTCGACGATGAGCG 135
Db 402 CCGGCTCCGAGACATGTCGG 422

RESULT 20
CNS030BV/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone 041B18 of library G from Tetraodon nigroviridis, genomic survey sequence.
AL253156
ACCESSION

VERSION
KEYWORDS
GSS: genome survey sequence.
SOURCE
ORGANISM
Tetraodon nigroviridis
Tetraodon nigroviridis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE
AUTHORS
1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
JOURNAL
MEDLINE
20296633
PUBMED
10835645
REFERENCE
AUTHORS
2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costraz,C., Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
JOURNAL
MEDLINE
20359837
PUBMED
10899143
COMMENT
TITLE
Genoscope.
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/Tetraodon>.
FEATURES
source
location/Qualifiers
1..627
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="041B18"
/clone_lib="G"
/note="Genoscope sequence ID : COBG041DA09LP1-end : T7"
ORIGIN
Query Match 23.5%; Score 36.2; DB 9; Length 627;
Best Local Similarity 68.5%; Pred. No. 38;
Matches 50; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 28 GTCGAGTGGGCGCGGAGCTGTCATCTGCTCATGTCGAGTGGGCGCGCGACTC 87
Db 414 GTCGAGGAGCGCGCGCGCTGCTGTCGCGCTGTCGAGAGAGTCTCCGCGAGCA 355
QY 88 GAGCATGAGGAG 100
Db 354 GACCATGAGGAG 342

RESULT 21
AZ933792
LOCUS
DEFINITION
BU-Ba0001B22F B. japonicum BAC library Bradyrhizobium japonicum genomic, genomic survey sequence.
AZ933792
VERSION
KEYWORDS
GSS.
SOURCE
ORGANISM
Bradyrhizobium japonicum
Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE
1 (bases 1 to 787)
Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,

Query Match	23.5%	Score 36.2	DB 9	Length 1057
Best Local Similarity	65.4%	Pred. No. 38		
Matches	53	Conservative 0	Mismatches 28	Indels 0
			Gaps 0	
Db	115	CCGCCGACTCGACGATGAGCG	135	
	558	CCGGCTCCCGACATGATCGCG	578	
RESULT 24				
LOCUS	CNS03W2P/c			
DEFINITION	Tetradodon nigroviridis genome survey sequence T7 end of clone 063118 of library G from Tetradodon nigroviridis, genomic survey sequence.			
ACCESSION	AL263194.1	GI:7984845		
VERSION	GSS: genome survey sequence.			
KEYWORDS	Tetradodon nigroviridis			
SOURCE	Tetradodon nigroviridis			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorphi; Acanthopterygii; Percomorphi; Tetraodontiformes; Tetraodontidae; Tetraodon.			
REFERENCE	1 Roest Crolius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fitzames,C., Wincker,P., Brotlier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetradodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)			
AUTHORS	2 Roest Crolius,H., Jalllon,O., Dasilva,C., Ozouf-Costaz,C., Fitzames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradodon nigroviridis Genome Res. 10 (7), 939-949 (2000)			
TITLE	JOURNAL			
JOURNAL	20296633			
MEDLINE	10835645			
PUBMED	3 (baaes 1 to 1057)			
REFERENCE	Genoscope.			
AUTHORS	Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail : sequefgenoscope.cns.fr			
JOURNAL	- web : www.genoscope.cns.fr)			
	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradodon nigroviridis genome. For more information, please take a look at			
	http://www.genoscope.cns.fr/Tetradodon.			
FEATURES	location/Qualifiers			
source	1..1057			
	/organism="Tetradodon nigroviridis"			
	/mol_type="Genomic DNA"			
	/db_xref="taxon:99883"			
	/clone="063118"			
	/clone_1lb="G"			
	/note="Genoscope sequence ID : COBG063B09LP1-end : T7"			
ORIGIN				
Query Match	23.5%	Score 36.2	DB 9	Length 1057
Best Local Similarity	65.4%	Pred. No. 38		
Matches	50	Conservative 0	Mismatches 23	Indels 0
			Gaps 0	
Db	28	GTCGAGTGGGCGCGGAGCTGATCTCGTATCGTGCAGTGGGCGCGCGGACTC	87	

LOCUS	DEFINITION	LOCUS	DEFINITION	LOCUS	DEFINITION
Db	570 GTCCGGAGCCGCGCCTGCTGTTCTTCGCGCCTGTCGAGAGCTCCTCGCCGAGGA 511	Oy	88 GACGATGAGCGAG 100 	Db	510 GACCATGAGCGAG 498
RESULT 25					
LOCUS	CO435934	862 bp	mrna	linear	EST 01-OCT-2000
DEFINITION	OsMR568 5MT resistant rice mutant cDNA library Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.				
ACCESSION	CO435934				
VERSION	CO435934.1	GI:53552954			
KEYWORDS	EST.				
ORGANISM	Oryza sativa (japonica cultivar-group)				
SOURCE	Oryza sativa (japonica cultivar-group)				
REFERENCE	1 (bases 1 to 862)				
AUTHORS	Kim,D.S., Lee,I.S., Kang,S.Y., Song,H.S., Lee,Y.I. and Seo,Y.W.				
TITLE	Expressed sequence tag (EST) analysis and characterization of differentially expressed genes related to 5-methyltryptophan (5MT) resistance in mutant rice				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Seo YW Department of Crop Science, division of Biotechnology and Genetic Engineering Korea University Anam-dong, Seongbuk-Gu, Seoul, 136-701, Korea Tel: +82 2 3290 3005 Fax: +82 2 3290 3501 Email: seoa@korea.ac.kr.				
FEATURES	location/Qualifiers				
source	1..862				
	/organism="Oryza sativa (japonica cultivar-group)"				
	/mol_type="mRNA"				
	/cultivar="Donganbyeon"				
	/db_xref="taxon:39947"				
	/tissue_type="5MT treated leaves, stems, and roots"				
	/dev_stage="seedling grown for 3 weeks"				
	/lab_host="XLI-Blue MRF"				
	/clone_id="5MT resistant rice mutant cDNA library"				
	/note="Vector: pBluescript SK4(+/-) phagemid. The rice mutant resistant to growth inhibition by 5MT were selected from the callus irradiated with gamma ray of 50 Gy through rice cv. Donganbyeon embryo culture. For construction of the cDNA library, 5MT resistant homologous rice mutants were treated by 5MT for 3 weeks."				
ORIGIN					
Query Match	23.4% Score 36; DB 7; Length 862;				
Best Local Similarity	54.5% Pred. No. 43;				
Matches	72; Conservative 0; Mismatches 60; Indels 0; Gaps 0				
Oy	18 CTCGCTCATCTCGAGTGGCGCGCGAGCTGTCATCTCGCTCATCTCGAGTGGCGG 77 	Db	139 CTGATAGATGATATACACAGGAGGACCGCGGTCTGCGCGCTCCCTCCGCGG 198 	Oy	78 CCGCGCATCTGACGATGAGGAGATGACAGCTCGCGCGCGCGCATGACGATGAGCGAG 137
Db	199 CCGCGCGCGCTCGCCACCCAAAGACGAGGTCTCGGCTACCGTCCGATCACATGACG 258 	Oy	138 ATGACGAGTCC 149 	Db	259 ACGACCAACACC 270
RESULT 26					
LOCUS	CO435934/c	862 bp	mrna	linear	EST 01-OCT-2000
DEFINITION	OsMR568 5MT resistant rice mutant cDNA library Oryza sativa				

(japonica cultivar-group) cDNA, mRNA sequence.
 ACCESSION CO435934
 VERSION CO435934.1 GI:53552954
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Euphorbiales; Oryzoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 862)
 AUTHORS Kim,D.S., Lee,I.S., Kang,S.Y., Song,H.S., Lee,Y.I. and Seo,Y.W.
 TITLE Expressed sequence tag (EST) analysis and characterization of differentially expressed genes related to 5-methyltryptophan (5MT) resistance in mutant rice
 JOURNAL Unpublished (2003)
 COMMENT Contact: Seo YW
 Department of Crop Science, division of Biotechnology and Genetic Engineering
 Korea University
 Anam-Dong, Seongbuk-Gu, Seoul, 136-701, Korea
 Tel: +82 2 3290 3005
 Fax: +82 2 3290 3501
 Email: seoag@korea.ac.kr.
 FEATURES
 source
 1..862
 Location/Qualifiers
 /organism="Oryza sativa (japonica cultivar-group)"
 /mol_type="mRNA"
 /cultiivar="Donghanbyeon"
 /db_xref="taxon:39947"
 /tissue_type="5MT treated leaves, stems, and roots"
 /dev_stage="seedling grown for 3 weeks"
 /lab_host="X11-Blue MRP"
 /clone_lib="5MT resistant rice mutant cDNA library"
 /note="Vector: pBluescript SK(+/-) phagemid; The rice mutant resistant to growth inhibition by 5MT were selected from the callus irradiated with gamma ray of 50 Gy through rice cv. Donghanbyeon embryo culture. For construction of the cDNA library, 5MT resistant homologous rice mutants were treated by 5MT for 3 weeks."
 ORIGIN
 Query Match 23.4%; Score 36; DB 7; Length 862;
 Best Local Similarity 54.5%; Pred. No. 43;
 Matches 72; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
 Oy 6 GGAGCTGTCATCTTCGCTCATGTCGAGTCGGCGCCGAGCTGTCATCTTCGCTCATCG 65
 Db 270 GGTGTGTGTCGTCGTCATGTCGATCGGAGCGGTACCGGAGACCGCTCTTGGTGGCG 211
 Oy 6 TCGAGTCGGCGCGCGCGAGCTCGACATGAGGAGATGACCACTCCGCGCGCGACTCG 125
 Db 210 AGGCGCGCGCGCGCGCGAGAGAGACCGGAGCGGAGCGGAGCGGAGCGGAGATCA 151
 Oy 126 ACGATGAGCGAG 137
 Db 150 TCACTGATGACG 139
 RESULT 27
 CNS04TDC 972 bp DNA linear GSS 01-SEP-2000
 LOCUS Tetradon nigroviridis genome survey sequence T3 end of clone 013112 of library A from Tetradon nigroviridis, genomic survey sequence.
 ACCESSION AL306353.1 GI:8204690
 VERSION AL306353.1
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetradon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradon.

REFERENCE
 AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W., and Weissenbach,J.
 TITLE Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
 MEDLINE 20296633
 PUBMED 10835645
 REFERENCE
 AUTHORS 2
 Roest Crolius,H., Jaillon,O., Dasilva,C., Orouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetradon nigroviridis
 JOURNAL Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837
 PUBMED 10899143
 REFERENCE
 AUTHORS 3 (bases 1 to 972)
 JOURNAL Genoscope.
 TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetradon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetradon.
 FEATURES
 source
 1..972
 Location/Qualifiers
 /organism="Tetradon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="013112"
 /clone_lib="A"
 /note="Genoscope sequence ID : CIAA0032E01A1-end : T3"
 ORIGIN
 Query Match 23.4%; Score 36; DB 9; Length 972;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 Oy 55 CTCGCTCATGTCGATCGGCGCGCGAGCTCGACATGAGCGAGATGACCACTCCG 114
 Db 474 CTCGCTCATGTCGTCGCGCGGAGAGCGTCTCGACAGCGGCGGAGAGAGCGG 533
 Oy 115 CCGCGACTCGACGATGAGGAGATGACCACTCC 149
 Db 534 CCGGCTCCCGGACATGTCGACCCAGAGAAAC 568
 RESULT 28
 CNS04TDC 972 bp DNA linear GSS 01-SEP-2000
 LOCUS Tetradon nigroviridis genome survey sequence T3 end of clone 013112 of library A from Tetradon nigroviridis, genomic survey sequence.
 ACCESSION AL306353.1 GI:8204690
 VERSION AL306353.1
 KEYWORDS GSS; genome survey sequence.
 SOURCE Tetradon nigroviridis
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetradon.
 REFERENCE
 AUTHORS 1
 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
 TITLE Estimate of human gene number provided by genome-wide analysis using Tetradon nigroviridis DNA sequence
 JOURNAL Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE 20296633
 PUBMED 10835645
 REFERENCE 2
 AUTHORS Reest Crollius H., Jallion O., Dasilva C., Ozouf-Costaz C., Fzames C., Fischer C., Bouneau L., Billaud A., Quetier F., Saurin W., Bernot A. and Weissenbach J.
 TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 JOURNAL Genome Res. 10 (7), 939-949 (2000)
 MEDLINE 20359837
 PUBMED 10899143
 REFERENCE 3 (bases 1 to 972)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 COMMENT BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
 FEATURES
 source 1. 972
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="013112"
 /clone_1lb="A"
 /note="Genoscope sequence ID : C1A0032E01A1-end : T3"
 ORIGIN
 Query Match 23.4%; Score 36; DB 9; Length 972;
 Best Local Similarity 60.0%; Pred. No. 42;
 Matches 57; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
 QY 6 GGAAGCTGATCTGCTCATCTGCTGAGTCGCGCGGAGAGCTGATCTGCTCATCG 65
 DB 568 GGTTCCTCTGCGGTCGAGCATGTCGCGGAGCCGCCCTTCTGTCNCGCCTGT 509
 QY 66 TCGAGTCGCGCGCGCGGAGTCGAGATGACGAG 100
 DB 508 CCGAGAGCTCTCCGCGAGCAGACATGAGCGAG 474
 RESULT 29
 BQ767987 367 bp mRNA linear EST 26-JUN-2002
 LOCUS EBR008_S0010_K07_R root, 3 week, drought-stressed, cv Optic, EBR008
 DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBR008_S0010_K07 5', mRNA
 sequence.
 ACCESSION BQ767987
 VERSION BQ767987.1 GI:21976461
 SOURCE Hordeum vulgare subsp. vulgare
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 367)
 REFERENCE Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L., Ramsay L., Machray G., Marshall D.F.M. and Waugh R.
 AUTHORS Development of Barley Transcriptome Resources
 TITLE Unpublished (2001)
 JOURNAL Contact: Waugh R, Marshall DF
 COMMENT Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.
 FEATURES
 source 1. 367
 /organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="EBR008_S0010_K07"
 /issue_type="root"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_1lb="root, 3 week, drought-stressed, cv Optic, EBR008"
 /note="Vector: pSPORT1; Site 1: Sal I; Site 2: Not I; Non-normalised library, directionally cloned into pSPORT1. Derived from roots of 3 week old drought stressed barley plants. Developed as part of the barley transcriptome resources of BBSRC/SERAD funded cereal IGF (Investigating Gene Function) project."
 ORIGIN
 Query Match 23.2%; Score 35.8; DB 5; Length 367;
 Best Local Similarity 55.1%; Pred. No. 49;
 Matches 70; Conservative 0; Mismatches 57; Indels 0; Gaps 0;
 QY 1 CGGCGGAGCTGTCATCTGCTCATCTGTCGAGTCGCGCGGAGCTGTCATCTGCT 60
 DB 220 CGGAGAGCGGCGCGGAGCAGACCGGAGGCCAGTCGTCCTCAACTCGACT 279
 QY 61 CATGTCGAGTCGCGCGCGCGGAGTCGAGATGACGAGATGACCACTCCGCGCG 120
 DB 280 GTCCTGGGCGCGCGCGGAGCAGACGCGAGCTGACCCGCTGCTGCTGCGCGCA 339
 QY 121 ACTGAC 127
 DB 340 CTCGCGC 346
 RESULT 30
 BQ767987/c 367 bp mRNA linear EST 26-JUN-2002
 LOCUS EBR008_S0010_K07_R root, 3 week, drought-stressed, cv Optic, EBR008
 DEFINITION Hordeum vulgare subsp. vulgare cDNA clone EBR008_S0010_K07 5', mRNA
 sequence.
 ACCESSION BQ767987
 VERSION BQ767987.1 GI:21976461
 SOURCE Hordeum vulgare subsp. vulgare
 KEYWORDS EST.
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Hordeum.
 1 (bases 1 to 367)
 REFERENCE Hedley P., Liu H., Caldwell D., McCallum N., Mudie S., Cardle L., Ramsay L., Machray G., Marshall D.F.M. and Waugh R.
 AUTHORS Development of Barley Transcriptome Resources
 TITLE Unpublished (2001)
 JOURNAL Contact: Waugh R, Marshall DF
 COMMENT Genome Dynamics/Computational Biology
 Scottish Crop Research Institute
 Invergowrie, Dundee, DD2 5DA, Scotland, UK
 Tel: 00 44 1382 562731
 Fax: 00 44 1382 562426
 Email: est@scri.sari.ac.uk.
 FEATURES
 source 1. 367
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="Optic"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="EBR008_S0010_K07"
 /issue_type="root"
 /dev_stage="3 week"
 /lab_host="DH10B"
 /clone_1lb="root, 3 week, drought-stressed, cv Optic, EBR008"

SOURCE
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
Eriocaulaceae; Oryzaceae; Oryza.
1 (bases 1 to 624)
Jantauriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)

TITLE
JOURNAL

COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1..624
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEF09L11"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

FEATURES
source

ORIGIN
Query Match 23.1%; Score 35.6; DB 6; Length 624;
Best Local Similarity 60.2%; Pred. No. 54;
Matches 59; Conservative 0; Mismatches 39; Indels 0; Gaps 0;
21 GCTCATGTCGACGTCGCGCGCGGAGCTGTCATCTGCTCATGTCGACGTCGCGCGG 80
287 GGTCTGCGACCGGATGCGCGGTCGCTCAACCCGCTGTCGCGCGCGCGCGCGG 346
81 CCGACTCGACGATGACGATGACCAAGCTCCGCGCG 118
347 CCGTCTCGGCTCCACCAAGAGTGGCTCCCGCGGAGC 384

RESULT 34
CB682412 624 bp mRNA linear EST 09-APR-2003
LOCUS OSJNEF09L11 f OSJNEF Oryza sativa (japonica cultivar-group) cDNA
DEFINITION clone OSJNEF09L11 5', mRNA sequence.
ACCESSION CB682412
VERSION CB682412.1 GI:29686137
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
Eriocaulaceae; Oryzaceae; Oryza.
1 (bases 1 to 624)
Jantauriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wang, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute

SOURCE
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 09 row: L column: 11
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1..624
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEF09L11"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

FEATURES
source

ORIGIN
Query Match 23.1%; Score 35.6; DB 6; Length 624;
Best Local Similarity 58.5%; Pred. No. 54;
Matches 62; Conservative 0; Mismatches 44; Indels 0; Gaps 0;
37 GCGCGCGGAGCTGTCATCTGCTCATGTCGACGTCGCGCGCGCGGATGAGTAC 96
384 GCTCCCGGAGGACCATCTTGTGTGACGCGGACGCGCGCGCGCGCGCGCGCGCG 325
97 CGAGATGACGACGTCGCGCGCGCGGACGTCGACGATGACGAGATGAC 142
324 CGGTTGAGCGGACCGCGCTGTCATCGCTCGGACGACCGCGCGGAGC 279

RESULT 35
CA198784 677 bp mRNA linear EST 25-SEP-2003
LOCUS SCCST3C12B03.g ST3 Saccharum officinarum cDNA clone SCCST3C12B03
DEFINITION 5', mRNA sequence.
ACCESSION CA198784
VERSION CA198784.1 GI:35230393
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 677)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUGEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genética
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parra@unilamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: C12 row: B column: 03
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..677
/organism="Saccharum officinarum"
/mol_type="mRNA"

FEATURES
source

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/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCCSTC312B03"
/lab_host="DH10B"
/clone_id="ST3"
note="Organ: Fourth apical internodes of adult

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/organism="Neurospora crassa"
/mol_type="mrna"
/strain="74-OR23-IV A (FGSC 2489) "
/db_xref="taxon:5141"
/clone="W01B11"
/sex="Mating type A"
/tissue_type="Unfertilized sexual tissue"
/dev_stage="unfertilized sexual stage"
/lab_host="E. coli"
/clone_alb="Westergaard"
note="Vector: plasmid SK (-); Site_1: EcoRI; Site_2:

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Db 384 GCCTGCACAGCGCGCATGCTCAGTGGC 412

RESULT 40
CA227997/c 704 bp mRNA linear EST 25-SEP-2003
LOCUS SCUFL3015B05.b Saccharum officinarum FL3 Saccharum officinarum
DEFINITION
ACCESSION
CDNA clone SCUFL3015B05 3', mRNA sequence.
CA227997
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Saccharum officinarum
Saccharum officinarum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.

REFERENCE
1 (bases 1 to 704)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
JOURNAL
COMMENT
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 015 row: B column: 05
Seq primer: SP6 Promoter primer.

FEATURES
source
1..704
Location/Qualifiers

/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCUFL3015B05"
/lab_host="DH10B"
/clone_lib="Saccharum officinarum FL3"
/note="Organ: Base of developing inflorescence (5cm-long);
vector: pSport1; Site 1: Salt; Site 2: NotI; An
unidirectional cDNA library generated from (Base of
developing inflorescence (5cm-long)). cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://succest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 23.0%; Score 35.4; DB 6; Length 704;
Best Local Similarity 53.2%; Pred. No. 61;
Matches 75; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
QY 13 GTCATCTGCTCATCTGATCGATCGCGCGCGAGCTGTCATCTCGCTCATCTCGCGATC 72
Db 404 GGCATTTGGCGCTGTGGACGGAGGGGTGCGCGAATGATGATCTTCGCTCGACGTTTGAA 345
QY 73 GCGCGCGCGCGCATCTGCAGATGAGCGAGATGACCATCGCTCCGCGCGCGCATCGACATGA 132
Db 344 GGAAGCCCTCTGCTGCTGCGCGGTGAGGAGACCGAGTGCAGACCCCGCGCGCGG 285
QY 133 GCGAGATGACGACGCTCCGCGCC 153
Db 284 GCTTCAAGCTTACGAGAGGCC 264

RESULT 41

BF483067

LOCUS BF483067 441 bp mRNA linear EST 06-DEC-2000
DEFINITION
WHE2314_D05 G10ZS wheat pre-anthesis spike cDNA library Triticum
aestivum CDNA clone WHE2314_D05_G10, mRNA sequence.
BF483067
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE
1 (bases 1 to 441)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
JOURNAL
COMMENT
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov

FEATURES
source
1..441
Location/Qualifiers

/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2314_D05_G10"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOUR"
/clone_lib="wheat pre-anthesis spike cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed. White, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared. A cDNA library was made, and
phagemids in the 10 close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN

Query Match 22.7%; Score 35; DB 2; Length 441;
Best Local Similarity 63.9%; Pred. No. 78;
Matches 53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 27 CGTGCAGTGGGCGCGCGAGCTGTCATCTCGCTCATCTGAGTGGCGCGCGACT 86
Db 20 CGTGCAGGCGGCGCGCGCGCGCTCTCTCTCTCTCGGCGGCGTCTGCGGCTT 79
QY 87 CGACGATGACGAGATGACCAACC 109
Db 80 CGGCGAGGGGCGACGCAACGCGC 102
RESULT 42
BF483067/c 441 bp mRNA linear EST 06-DEC-2000
LOCUS BF483067
DEFINITION
WHE2314_D05 G10ZS wheat pre-anthesis spike cDNA library Triticum
aestivum CDNA clone WHE2314_D05_G10, mRNA sequence.
BF483067
ACCESSION
VERSION
KEYWORDS
EST.

SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum
REFERENCE AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 441) Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Heis,C.C., Kang,Y., Lazo,G.R., Miller,R., Rauech,C.J., Seaton,C.L. and Tong,J.C.
JOURNAL COMMENT	The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library unpublished (2000) Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel.: 5105595773 Fax: 5105595818 Email: oanderson@pw.usda.gov
FEATURES	Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: StrataGene SK primer. Location/Qualifiers 1..441 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="WHE2314.D05.G10" /tissue_type="Spike before anthesis" /dev_stage="Adult plant" /lab_host="E. coli SOLR" /clone_id="Wheat pre-anthesis spike cDNA library" /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give plasmid script phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
ORIGIN	
Query Match	22.7%; Score 35; DB 2; Length 441;
Best Local Similarity	63.9%; Pred. No. 78;
Matches	53; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
OY	46 GCTGTCATCTCGCTCATCTGTGAGTGGCGGCCGCAGCTCGACGATGACGAGATGAC 105 Db 102 GCCGTGCGCCGTGCGCCCTCGCGCAAGCCGCGGAGCGCCGCCGAGAGAGAGAGAG 43
OY	106 CAGCTCGCGCGCGCGAGCTCGACG 128
Db	42 GACGCGCGCGCGCGCGCTCGACG 20
RESULT 43	
LOCUS	BO805125 571 bp mRNA linear EST 31-JUL-2002
DEFINITION	WH3553_B09.C17S5 Wheat developing grains cDNA library Triticum
ACCESSION	BO805125
VERSION	BO805125.1 GI:22029334
KEYWORDS	EST.
SOURCE	Triticum aestivum (bread wheat)
ORGANISM	Triticum aestivum
REFERENCE AUTHORS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum. 1 (bases 1 to 571) Altenbach,S., Anderson,O.D., Chao,S., Chin,A., Close,T.J.,

TITLE	Cronin,K., Crossman,C., Fenton,R.D., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.
JOURNAL COMMENT	The structure and function of the expressed portion of the wheat genomes - Developing grains cdna library Unpublished (2002) Contact: Olin Anderson US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: oanderson@wp.usda.gov Sequences have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: SK primer. Location/Qualifiers
FEATURES	
source	1..571 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Butte 86" /db_xref="taxon:4565" /clone="WHEJ3563_B09_C17" /tissue_type="whole grains" /dev_stage="3-44 days post anthesis seed" /lab_host="B. coli SOLR" /clone_lib="wheat developing grains cdna library" /note="Vector: Lambda ZAP II, excised phagemid; Site_1: EcoRI; Plants were grown under six following different environmental regimes in greenhouse, Environment 1) 24oc/17oc day/night, well-watered, with post-anthesis fertilizer, Environment 2) 24oc/17oc day/night, well-watered, without post-anthesis fertilizer, Environment 3) 37oc/17oc day/night, well-watered, with post-anthesis fertilizer, Environment 4) 37oc/17oc day/night, well-watered, without post-anthesis fertilizer, Environment 5) 37oc/17oc day/night plus drought, with post-anthesis fertilizer, Environment 6) 37oc/17oc day/night plus drought, without post-anthesis fertilizer, developing wheat grains from the following were excised and frozen in liquid nitrogen, Environment 1 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA library was made using poly (A) RNA, and the cDNA clones were in vivo excised to give plasmid (SK-) phagemids in the TV Close lab (Chin, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (others)."
ORIGIN:	
Query Match	22.7%; Score 35; DB 5; Length 571;
Best Local Similarity	63.9%; Pred. No. 77;
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Dd	116 CATTGAGACGGCGGCCCGCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 175
Gy	87 CGACGATGAGCGAGATGACCAGC 109
Dd	176 CGGCCAGGGCGACGCGCACGCGC 198
RESULT 44	BGB0805125
LOCUS	BGB0805125
DEFINITION	WHEJ3563_B09_C17S Wheat developing grains cdna library Triticum
	571 bp mRNA linear EST 31-Jul-2002

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:20:25 ; Search time 504 Seconds
(without alignments)
1851.668 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154

Sequence: 1 cggcgcgagctgtcatctc.....gagatgacagctccgcgcg 154

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5615251 seqs, 3030001701 residues

Total number of hits satisfying chosen parameters: 11230502

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database :

Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US10F_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	10	US-09-887-194A-13
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3	154	100.0	154	10	US-09-887-194A-13
4	154	100.0	154	10	US-09-934-900-25
5	154	100.0	154	10	US-09-934-900-25
6	154	100.0	154	18	US-10-734-947-7
7	154	100.0	154	18	US-10-734-947-7
8	154	100.0	154	19	US-10-981-293-25
9	154	100.0	154	19	US-10-981-293-25
10	154	100.0	154	17	US-10-459-159-1
11	154	100.0	154	17	US-10-459-159-1

12	154	100.0	7701	17	US-10-427-570A-9	Sequence 9, Appl1
13	154	100.0	7701	18	US-10-734-947-1	Sequence 1, Appl1
14	154	100.0	7701	18	US-10-734-947-1	Sequence 1, Appl1
15	112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appl1
16	112	72.7	4974	9	US-09-906-209-17	Sequence 17, Appl1
17	82.8	53.8	6611	10	US-09-934-900-26	Sequence 26, Appl1
18	82.8	53.8	6611	10	US-09-934-900-26	Sequence 26, Appl1
19	82.8	53.8	6611	19	US-10-981-293-26	Sequence 26, Appl1
20	82.8	53.8	6611	19	US-10-981-293-26	Sequence 26, Appl1
21	81	52.6	963	10	US-09-887-194A-29	Sequence 29, Appl1
22	81	52.6	963	10	US-09-887-194A-29	Sequence 29, Appl1
23	80	51.9	80	10	US-09-887-194A-12	Sequence 12, Appl1
24	80	51.9	80	10	US-09-887-194A-12	Sequence 12, Appl1
25	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appl1
26	80	51.9	80	10	US-09-934-900-24	Sequence 24, Appl1
27	80	51.9	80	19	US-10-981-293-24	Sequence 24, Appl1
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29	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl1
30	80	51.9	92	10	US-09-887-194A-14	Sequence 14, Appl1
31	45.8	29.7	1717	10	US-09-887-194A-24	Sequence 24, Appl1
32	45.8	29.7	1717	10	US-09-887-194A-24	Sequence 24, Appl1
33	38.2	24.8	1251	17	US-10-389-647-277	Sequence 277, App
34	38.2	24.8	1251	17	US-10-389-647-277	Sequence 277, App
35	38	24.7	1581	15	US-10-156-761-6327	Sequence 6327, Ap
36	38	24.7	1581	15	US-10-156-761-6327	Sequence 6327, Ap
37	38	24.7	9025608	15	US-10-156-761-1	Sequence 1, Appl1
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39	37	24.0	1821	18	US-10-437-963-43250	Sequence 43250, A
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45	36	23.4	816	18	US-10-437-963-36912	Sequence 36912, A
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47	36	23.4	1153	18	US-10-425-115-141776	Sequence 141776, A
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55	35.2	22.9	2730	17	US-10-260-238-1055	Sequence 1055, Ap
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57	35	22.7	850	16	US-10-029-386-24874	Sequence 24874, A
58	35	22.7	850	16	US-10-029-386-24874	Sequence 24874, A
59	34.8	22.6	903	15	US-10-156-761-5558	Sequence 5558, Ap
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61	34.8	22.6	1681	16	US-10-271-889-7	Sequence 7, Appl1
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63	34.6	22.5	1217	18	US-10-437-963-96989	Sequence 96989, A
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65	34.4	22.3	1699	18	US-10-437-963-52771	Sequence 52771, A
66	34.4	22.3	1699	18	US-10-437-963-52771	Sequence 52771, A
67	34.2	22.2	366	18	US-10-437-963-72120	Sequence 72120, A
68	34.2	22.2	366	18	US-10-437-963-72120	Sequence 72120, A
69	34.2	22.2	968	18	US-10-739-930-4744	Sequence 4744, Ap
70	34.2	22.2	968	18	US-10-739-930-4744	Sequence 4744, Ap
71	34.2	22.2	1245	17	US-10-260-238-3694	Sequence 3694, Ap
72	34.2	22.2	1245	17	US-10-260-238-3694	Sequence 3694, Ap
73	34	22.1	1775	18	US-10-437-963-51378	Sequence 51378, A
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75	34	22.1	1786	18	US-10-437-963-68140	Sequence 68140, A
76	34	22.1	1786	18	US-10-437-963-68140	Sequence 68140, A
77	34	22.1	4758	18	US-10-437-963-97719	Sequence 97719, A
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79	33.8	21.9	846	18	US-10-437-963-61	Sequence 61, Appl1
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81	33.8	21.9	1386	17	US-10-104-047-1062	Sequence 1062, Ap
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83	33.8	21.9	2100	18	US-10-437-963-330	Sequence 330, App
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88 33.8 21.9 3107 9 US-09-812-350-39
89 33.6 21.8 726 18 US-10-437-963-37821
90 33.6 21.8 726 18 US-10-437-963-37821
91 33.6 21.8 1233 17 US-10-282-122A-26073
92 33.6 21.8 1233 17 US-10-282-122A-26073
93 33.4 21.7 1105 17 US-10-282-122A-11328
94 33.4 21.7 1105 17 US-10-282-122A-11328
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98 33.4 21.7 1574 17 US-10-115-831-157
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ALIGNMENTS

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Sequence 40, Appl.
Sequence 40, Appl.
Sequence 39, Appl.
Sequence 39, Appl.
Sequence 37821, A
Sequence 26073, A
Sequence 26073, A
Sequence 11328, A
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Sequence 60837, A
Sequence 60837, A
Sequence 157, App
Sequence 157, App
Sequence 100458,
Sequence 100458,

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RESULT 1

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; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.
; APPLICANT: Nicholas, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: B81449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-13

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Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 1 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 60
Qy 61 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 120
Db 61 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 120
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Db 121 ACTGACGATGAGCGAGATGACCAAGCTCCGGCCG 154

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RESULT 2

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US-09-887-194A-13/c
; Sequence 13, Application US/09887194A
; Publication No. US20030036197A1
; GENERAL INFORMATION:
; APPLICANT: Glassman, Kimberly F.
; APPLICANT: Gordon-Kamm, William J.
; APPLICANT: Kinney, Anthony
; APPLICANT: Lowe, Keith S.

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; APPLICANT: Nichols, Scott E.
; APPLICANT: Stecca, Kevin L.
; TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
; FILE REFERENCE: B81449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-13

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Query Match 100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 120
Db 94 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 35
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RESULT 3

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; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Canoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: B81476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-934-900-25

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Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 1 CGGCGGAGCTGTCATCTGCTCATCTGTCAGTCGGCGCGGAGCTGTCATCTGCT 60
Qy 61 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 120
Db 61 CATGTCGAGTCGGCGCGCGCGGAGCTGTCAGTCGAGTCGAGTCACCAAGCTCCGGCCG 120

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Oy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154

RESULT 4

US-09-934-900-25/c
; Sequence 25, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booch, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadau, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-934-900-25

Query Match 100.0%; Score 154; DB 10; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGCTCATCTCGCT 60
Db 154 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGCTCATCTCGCT 95
Oy 61 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 120
Db 94 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 35
Oy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 34 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 1

RESULT 5

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; Sequence 7, Application US/10734947
; Publication No. US20040128714A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIDITIGENIN-DERIVED ISOPHAVONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOPHAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
; FILE REFERENCE: BB1535 US NA
; CURRENT APPLICATION NUMBER: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two

OTHER INFORMATION: 36-nucleotide repeats and having an EagI site at each end.
US-10-734-947-7

Query Match 100.0%; Score 154; DB 18; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGCTCATCTCGCT 60
Oy 61 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 120
Db 61 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 120
Oy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154

RESULT 6

US-10-734-947-7/c
; Sequence 7, Application US/10734947
; Publication No. US20040128714A1
; GENERAL INFORMATION:
; APPLICANT: McGonigle, Brian
; TITLE OF INVENTION: METHOD OF DECREASING LIQUIDITIGENIN-DERIVED ISOPHAVONES RELATIVE
; TITLE OF INVENTION: TOTAL ISOPHAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
; FILE REFERENCE: BB1535 US NA
; CURRENT APPLICATION NUMBER: US/10/734,947
; PRIOR FILING DATE: 2003-12-11
; PRIOR APPLICATION NUMBER: US 60/433,433
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence containing a NotI site flanked by two
US-10-734-947-7

Query Match 100.0%; Score 154; DB 18; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGCTCATCTCGCT 60
Db 154 CGGCGGAGCTGCTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGCTCATCTCGCT 95
Oy 61 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 120
Db 94 CATGTCGAGTCGGCGCGGCGGAGCTGAGATGAGGAGATGAGACCAAGCTCCGGCGCG 35
Oy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 154
Db 34 ACTGACGATGAGGAGATGACCAAGCTCCGGCG 1

RESULT 7

US-10-981-293-25
; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booch, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadau, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-

```

; TITLE OF INVENTION: ACP Desaturase
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; US-10-981-293-25

```

```

Query Match          100.0%; Score 154; DB 19; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 60
        |||
DB      1 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 60
        |||

QY      61 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
        |||
DB      61 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
        |||

QY      121 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 154
        |||
DB      121 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 154
        |||

```

```

RESULT 8
US-10-981-293-25/c
; Sequence 25, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hitz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadev, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 25
; LENGTH: 154
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS133
; US-10-981-293-25

```

```

Query Match          100.0%; Score 154; DB 19; Length 154;
Best Local Similarity 100.0%; Pred. No. 2.2e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

1 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 60
154 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 95

```

QY      61 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
        |||
DB      94 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 35
        |||

QY      121 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 154
        |||
DB      34 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 1
        |||

```

```

RESULT 9
US-10-459-159-1
; Sequence 1, Application US/10459159
; Publication No. US20040006795A1
; GENERAL INFORMATION:
; APPLICANT: Mcgonigle, Brian
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: METHOD TO INCREASE THE ISOFLAVONOID LEVELS IN PLANTS AND PLANTS
; FILE REFERENCE: BB1526 US NA
; CURRENT APPLICATION NUMBER: US/10/459,159
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 60/388,280
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: expression vector pKS151
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (6516) ..(6516)
; OTHER INFORMATION: n = A, C, G, or T
; US-10-459-159-1

```

```

Query Match          100.0%; Score 154; DB 17; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 60
        |||
DB      5451 CGGCGGAGCTGCTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTCGCT 5510
        |||

QY      61 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
        |||
DB      5511 CATGTCGAGTCGGGGCGCGCGGAGCTCGACGATGAGCGAGATGACCACTCCGGCGCG 5570
        |||

QY      121 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 154
        |||
DB      5571 ACTGACGATGAGCGAGATGAGCACTCCGGCGCG 5604
        |||

```

```

RESULT 10
US-10-459-159-1/c
; Sequence 1, Application US/10459159
; Publication No. US20040006795A1
; GENERAL INFORMATION:
; APPLICANT: Mcgonigle, Brian
; APPLICANT: Odell, Joan T.
; TITLE OF INVENTION: METHOD TO INCREASE THE ISOFLAVONOID LEVELS IN PLANTS AND PLANTS
; FILE REFERENCE: BB1526 US NA
; CURRENT APPLICATION NUMBER: US/10/459,159
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: 60/388,280
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 7701
; TYPE: DNA
; ORGANISM: expression vector pKS151

```


FEATURE:
NAME/KEY: misc feature
LOCATION: (6516)..
OTHER INFORMATION: n = A, C, G, or T
US-10-459-159-1

Query Match
Best Local Similarity 100.0%; Score 154; DB 17; Length 7701;
Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
DB 5604 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 5545
QY 61 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 120
DB 5544 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 5485
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 154
DB 5484 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 5451

RESULT 11
US-10-427-570A-9
Sequence 9, Application US/10427570A
Publication No. US20040010818A1

GENERAL INFORMATION:
APPLICANT: McGonigle, Brian
APPLICANT: Maxwell, Carl A.
APPLICANT: Hession, Aileen O.
TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
FILE REFERENCE: BB1523 US NA
CURRENT APPLICATION NUMBER: US/10/427,570A
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: expression vector pKS151
FEATURE:
NAME/KEY: Unsure
LOCATION: (6516)
OTHER INFORMATION: n = A, C, G, or T
US-10-427-570A-9

Query Match
Best Local Similarity 100.0%; Score 154; DB 17; Length 7701;
Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
DB 5451 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 5510
QY 61 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 120
DB 5511 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 5570
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 154
DB 5571 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 5604

RESULT 12
US-10-427-570A-9/c
Sequence 9, Application US/10427570A
Publication No. US20040010818A1
GENERAL INFORMATION:

APPLICANT: McGonigle, Brian
APPLICANT: Maxwell, Carl A.
APPLICANT: Hession, Aileen O.
TITLE OF INVENTION: TRANSGENIC PLANTS WITH A SUPPRESSED TRITERPENE LEVEL
FILE REFERENCE: BB1523 US NA
CURRENT APPLICATION NUMBER: US/10/427,570A
CURRENT FILING DATE: 2003-05-01
PRIOR APPLICATION NUMBER: 60/379,361
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Microsoft Office 97
SEQ ID NO 9
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: expression vector pKS151
FEATURE:
NAME/KEY: Unsure
LOCATION: (6516)
OTHER INFORMATION: n = A, C, G, or T
US-10-427-570A-9

Query Match
Best Local Similarity 100.0%; Score 154; DB 17; Length 7701;
Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
DB 5604 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 5545
QY 61 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 120
DB 5544 CATGTCGAGTCGGCGCGCGCGAGTCCAGATGAGCGAGTCCAGCTCCGCGCGCG 5485
QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 154
DB 5484 ACTCGACGATGAGCGAGATGACCAAGCTCCGCGCG 5451

RESULT 13
US-10-734-947-1
Sequence 1, Application US/10734947
Publication No. US20040128714A1

GENERAL INFORMATION:
APPLICANT: McGonigle, Brian
TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: BB1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Expression Vector pKS151
FEATURE:
NAME/KEY: misc feature
LOCATION: (6516)..
OTHER INFORMATION: n = A, C, G, or T
US-10-734-947-1

Query Match
Best Local Similarity 100.0%; Score 154; DB 18; Length 7701;
Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTGGCGCGGAGCTGTCATCTCGCT 60

Db 5451 CCGCGGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGCGGAGCTGATCTGCT 5510
Qy 61 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 120
Db 5511 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 5570
Qy 121 ACTGACGATGAGCGAGATGACCACTCCGCGCG 154
Db 5571 ACTGACGATGAGCGAGATGACCACTCCGCGCG 5604

RESULT 14
US-10-734-947-1/c
Sequence 1, Application US/10734947
Publication No. US20040128714A1

GENERAL INFORMATION:
APPLICANT: McGenigle, Brian
TITLE OF INVENTION: METHOD OF DECREASING LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE
TITLE OF INVENTION: TOTAL ISOFLAVONES IN PLANTS AND PLANTS PRODUCING REDUCED RATIO C
TITLE OF INVENTION: LIQUIRITIGENIN-DERIVED ISOFLAVONES RELATIVE TO TOTAL ISOFLAVONES
FILE REFERENCE: B1535 US NA
CURRENT APPLICATION NUMBER: US/10/734,947
CURRENT FILING DATE: 2003-12-11
PRIOR APPLICATION NUMBER: US 60/433,433
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Microsoft Office 97
SEQ ID NO 1
LENGTH: 7701
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Expression Vector pKS151
FEATURE:
NAME/KEY: misc feature
LOCATION: (6516)..(6516)
OTHER INFORMATION: n = A, C, G, or T
US-10-734-947-1

Query Match 100.0%; Score 154; DB 18; Length 7701;
Best Local Similarity 100.0%; Pred. No. 1.8e-37;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGGAGCTGATCTGCT 60
Db 5604 CCGCGGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGGAGCTGATCTGCT 5545
Qy 61 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 120
Db 5544 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 5485
Qy 121 ACTGACGATGAGCGAGATGACCACTCCGCGCG 154
Db 5484 ACTGACGATGAGCGAGATGACCACTCCGCGCG 5451

RESULT 15
US-09-906-209-17
Sequence 17, Application US/09906209
Patent No. US20020165385A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Ilaag, Lawrence L.
TITLE OF INVENTION: Plasmidic Phosphoglucomutase Genes
FILE REFERENCE: B1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17

SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 4974
TYPE: DNA
ORGANISM: synthetic construct
FEATURE:
NAME/KEY: unsure
LOCATION: (3951)
OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match 72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 9.8e-25;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGCGGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGGAGCTGATCTGCT 60
Db 4863 CCGCGGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGGAGCTGATCTGCT 4922
Qy 61 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCC 112
Db 4923 CATGCTGAGTGGCGCGCGCGGAGCTGAGATGAGGAGTACCACTCC 4974

RESULT 16
US-09-906-209-17/c
Sequence 17, Application US/09906209
Patent No. US20020165385A1

GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Butler, Karla
APPLICANT: Carlson, Tom
APPLICANT: Ilaag, Lawrence L.
TITLE OF INVENTION: Plasmidic Phosphoglucomutase Genes
FILE REFERENCE: B1451 NA
CURRENT APPLICATION NUMBER: US/09/906,209
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 60/218,712
PRIOR FILING DATE: JULY 17, 2000
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Microsoft Office 97
SEQ ID NO 17
LENGTH: 4974
TYPE: DNA
ORGANISM: synthetic construct
FEATURE:
NAME/KEY: unsure
LOCATION: (3951)
OTHER INFORMATION: n = A, C, G, or T
US-09-906-209-17

Query Match 72.7%; Score 112; DB 9; Length 4974;
Best Local Similarity 100.0%; Pred. No. 9.8e-25;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGCGGAGCTGAGATGAGGAGT 102
Db 4974 GGAGCTGGTCACTCTGCTCATCTGAGTGGCGCGCGGAGCTGAGATGAGGAGT 4915
Qy 103 GACCACTCCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 154
Db 4914 GACCACTCCGCGCGCGGAGCTGAGATGAGGAGTACCACTCCGCGCG 4863

RESULT 17
US-09-934-900-26
Sequence 26, Application US/09934900
Publication No. US20030054521A1
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Canoon, Rebecca B
APPLICANT: Hitz, William D
APPLICANT: Kinney, Anthony

APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
FEATURE:
NAME/KEY: Unsure
LOCATION: (4436) ..(4436)
OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match 53.8%; Score 82.8; DB 10; Length 6611;
Best Local Similarity 97.7%; Pred. No. 7e-16;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGGCGGAGCTGCTCATCTGCT 60
Db 5348 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGGCGGAGCTGCTCATCTGCT 5407
Qy 61 CATCTGAGTGGCGGCGCGCGAGCT 86
Db 5408 CATCTGAGTGGCGGCGCGCGAGT 5433

RESULT 18
US-09-934-900-26/c
Sequence 26, Application US/09934900
Publication No. US20030054521A1
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hiltz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/09/934,900
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
FEATURE:
NAME/KEY: Unsure
LOCATION: (4436) ..(4436)
OTHER INFORMATION: n = A, C, G, or T
US-09-934-900-26

Query Match 53.8%; Score 82.8; DB 10; Length 6611;
Best Local Similarity 97.7%; Pred. No. 7e-16;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 69 AGTGGGCGGCGCGGAGCTGCGAGTGGAGCGGAGCTGCGGCGGAGCTGCGAGC 128
Db 5433 ACTAGGCGGCGCGGAGCTGCGAGTGGAGCGGAGTGGAGCTGCGGCGGAGCTGCGAGC 5374
Qy 129 ATGAGCGAGTGGAGCTGCGGCGG 154
Db 5373 ATGAGCGAGTGGAGCTGCGGCGG 5348

RESULT 19
US-10-981-293-26
Sequence 26, Application US/10981293
Publication No. US20050066390A1
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hiltz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
FEATURE:
NAME/KEY: Unsure
LOCATION: (4436) ..(4436)
OTHER INFORMATION: n = A, C, G, or T
US-10-981-293-26

Query Match 53.8%; Score 82.8; DB 19; Length 6611;
Best Local Similarity 97.7%; Pred. No. 7e-16;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGGCGGAGCTGCTCATCTGCT 60
Db 5348 CGGCGGAGCTGCTCATCTGCTCATCTGCTGCGGCGGAGCTGCTCATCTGCT 5407
Qy 61 CATCTGAGTGGCGGCGCGCGAGCT 86
Db 5408 CATCTGAGTGGCGGCGCGCGAGT 5433

RESULT 20
US-10-981-293-26/c
Sequence 26, Application US/10981293
Publication No. US20050066390A1
GENERAL INFORMATION:
APPLICANT: Booth, Russ
APPLICANT: Cahoon, Rebecca E
APPLICANT: Hiltz, William D
APPLICANT: Kinney, Anthony
APPLICANT: Yadav, Naren
TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
FILE REFERENCE: BB1476 US NA
CURRENT APPLICATION NUMBER: US/10/981,293
CURRENT FILING DATE: 2004-11-04
PRIOR APPLICATION NUMBER: US/09/934,900
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/226996
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 6611
TYPE: DNA
ORGANISM: Plasmid pBS68
FEATURE:
NAME/KEY: Unsure

```

; APPLICANT: Stecca, Kevin L.

```

```
; FILE REFERENCE: BB1449 US NA
; CURRENT APPLICATION NUMBER: US/09/887,194A
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 12
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; US-09-887-194A-12
```

```
Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 38 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 80 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21
Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 20 GAGATGACCAAGCTCCGGCCG 1
```

```
RESULT 25
US-09-934-900-24
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS106 and pKS124
; US-09-934-900-24
```

```
Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 38 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 1 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 60
Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 61 GAGATGACCAAGCTCCGGCCG 80
```

```
RESULT 26
US-09-934-900-24/c
; Sequence 24, Application US/09934900
; Publication No. US20030054521A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/09/934,900
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS106 and pKS124
; US-09-934-900-24
```

```
Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 38 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 80 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 21
Qy 98 GAGATGACCAAGCTCCGGCCG 117
Db 20 GAGATGACCAAGCTCCGGCCG 1
```

```
RESULT 27
US-10-981-293-24
; Sequence 24, Application US/10981293
; Publication No. US20050066390A1
; GENERAL INFORMATION:
; APPLICANT: Booth, Russ
; APPLICANT: Cahoon, Rebecca E
; APPLICANT: Hiltz, William D
; APPLICANT: Kinney, Anthony
; APPLICANT: Yadav, Naren
; TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-
; FILE REFERENCE: BB1476 US NA
; CURRENT APPLICATION NUMBER: US/10/981,293
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/934,900
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/226996
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 80
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
; OTHER INFORMATION: region of pKS106 and pKS124
; US-10-981-293-24
```

```
Query Match          51.9%; Score 80; DB 10; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 38 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 97
Db 1 CGGCGGAGCTGTGTCATCTCGCTCATGTCGAGTCGGCGCGCCGCACTCGACGATGAGC 60
```

OY 98 GAGATGACCACTCCGGCCG 117
|
Db 61 GAGATGACCACTCCGGCCG 80

RESULT 28
US-10-981-293-24/c

Sequence 24, Application US/10981293
Publication No. US20050066390A1

GENERAL INFORMATION:

APPLICANT: Booth, Russ

APPLICANT: Canoon, Rebecca E

APPLICANT: Hitz, William D

APPLICANT: Kinney, Anthony

APPLICANT: Yaday, Naren

TITLE OF INVENTION: Nucleotide Sequences of a New Class of Diverged Delta-9 Stearoyl-

TITLE OF INVENTION: ACP Desaturase

FILE REFERENCE: BBI476 US NA

CURRENT APPLICATION NUMBER: US/10/981,293

PRIOR FILING DATE: 2004-11-04

PRIOR APPLICATION NUMBER: US/09/934,900

PRIOR FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/226996

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Microsoft Office 97

SEQ ID NO: 24

LENGTH: 80

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary

US-10-981-293-24

Query Match 51.9%; Score 80; DB 19; Length 80;
Best Local Similarity 100.0%; Pred. No. 6.3e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGACTCGACGATGAGC 97
|
Db 80 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGACTCGACGATGAGC 21

OY 98 GAGATGACCACTCCGGCCG 117
|
Db 20 GAGATGACCACTCCGGCCG 1

RESULT 29
US-09-887-194A-14

Sequence 14, Application US/09887194A

Publication No. US20030036197A1

GENERAL INFORMATION:

APPLICANT: Glassman, Kimberly F.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Kinney, Anthony

APPLICANT: Lowe, Keith S.

APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

FILE REFERENCE: BBI449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO: 14

LENGTH: 92

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES PCR primer

US-09-887-194A-14

Query Match 51.9%; Score 80; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGCGACTCGACGATGAGC 97
|
Db 7 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGCGACTCGACGATGAGC 66

OY 98 GAGATGACCACTCCGGCCG 117
|
Db 67 GAGATGACCACTCCGGCCG 86

RESULT 30
US-09-887-194A-14/c

Sequence 14, Application US/09887194A

Publication No. US20030036197A1

GENERAL INFORMATION:

APPLICANT: Glassman, Kimberly F.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Kinney, Anthony

APPLICANT: Lowe, Keith S.

APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

FILE REFERENCE: BBI449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO: 14

LENGTH: 92

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES PCR primer

US-09-887-194A-14

Query Match 51.9%; Score 80; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 6.2e-15;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGCGACTCGACGATGAGC 97
|
Db 86 CGGCGGAGCTGTGTCATCTGCTCATCTGAGTCGGCGCCGCGCGACTCGACGATGAGC 27

OY 98 GAGATGACCACTCCGGCCG 117
|
Db 26 GAGATGACCACTCCGGCCG 7

RESULT 31
US-09-887-194A-24

Sequence 24, Application US/09887194A

Publication No. US20030036197A1

GENERAL INFORMATION:

APPLICANT: Glassman, Kimberly F.

APPLICANT: Gordon-Kamm, William J.

APPLICANT: Kinney, Anthony

APPLICANT: Lowe, Keith S.

APPLICANT: Nichols, Scott E.

APPLICANT: Stecca, Kevin L.

TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION

FILE REFERENCE: BBI449 US NA

CURRENT APPLICATION NUMBER: US/09/887,194A

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 36

SOFTWARE: Microsoft Office 97

SEQ ID NO: 24

LENGTH: 1717

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES PCR primer

US-09-887-194A-14

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
OTHER INFORMATION: region of pBS68
US-09-887-194A-24

Query Match 29.7%; Score 45.8; DB 10; Length 1717;
Best Local Similarity 95.9%; Pred. No. 0.00013;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 38 CGGCGGAGCTGCTCATCTCGTCCATCGAGTGGGCGCGCGGACT 86
1 CGGCGGAGCTGCTCATCTCGTCCATCGAGTGGGCGCGCGGACT 49

RESULT 32
US-09-887-194A-24/c
Sequence 24, Application US/09887194A
Publication No. US20030036197A1
GENERAL INFORMATION:
APPLICANT: Glaesman, Kimberly F.
APPLICANT: Gordon-Kamm, William J.
APPLICANT: Kinney, Anthony
APPLICANT: Lowe, Keith S.
APPLICANT: Nicolls, Scott E.
APPLICANT: Stecca, Kevin L.
TITLE OF INVENTION: RECOMBINANT CONSTRUCTS AND THEIR USE IN REDUCING GENE EXPRESSION
FILE REFERENCE: B01449 US NA
CURRENT APPLICATION NUMBER: US/09/887,194A
PRIOR FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 24
LENGTH: 1717
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: ELVISLIVES complementary
US-09-887-194A-24

Query Match 29.7%; Score 45.8; DB 10; Length 1717;
Best Local Similarity 95.9%; Pred. No. 0.00013;
Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 69 AGTGGCGGCGCGCGGCTCGAGATGACGAGATACCACTCCGCGCG 117
49 ACTAGCGGCGCGCGGCTCGAGATGACGAGATACCACTCCGCGCG 1

RESULT 33
US-10-389-647-277
Sequence 277, Application US/10389647
Publication No. US2004003549A1
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: U12-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/153022
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 277
LENGTH: 1251
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-389-647-277

Query Match 24.8%; Score 38.2; DB 17; Length 1251;
Best Local Similarity 61.6%; Pred. No. 0.026;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Db 37 GCGCGGAGCTGCTCATCTCGTCCATCGAGTGGGCGCGCGGACTGAG 96
1080 GCTGCTGATGATCTGTCACCCCGCACCTGCTCCAGCCGCGCGGAGTTC 1139
Qy 97 CGAGATGACGACGCTCCGCGCGCGGACTCGAGATGAGG 135
Db 1140 GAACTGCGCGGCGAGGCGCTGCGGCACTAGATCCGG 1178

RESULT 34
US-10-389-647-277/c
Sequence 277, Application US/10389647
Publication No. US2004003549A1
GENERAL INFORMATION:
APPLICANT: GREENBERG, E. Peter
APPLICANT: SCHUSTER, Martin
APPLICANT: LOSTROH, Candi
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: U12-038CP
CURRENT APPLICATION NUMBER: US/10/389,647
PRIOR FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 09/653730
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/153022
NUMBER OF SEQ ID NOS: 710
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 277
LENGTH: 1251
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-10-389-647-277

Query Match 24.8%; Score 38.2; DB 17; Length 1251;
Best Local Similarity 61.6%; Pred. No. 0.026;
Matches 61; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
Db 20 CGCTCATGCTGAGTGGCGCGCGGAGCTGCTCATCTGCTCATGCTGAGTGGCGGCG 79
1178 CCCGATGCTGCTGCTGCGGAGGCTCTCGCGGCGAGTCCGCACTGCTGCGGCGCG 1119
Qy 80 GCCGACTGACGATGAGCGAGATGACGACTCCGCGCGCG 118
Db 1118 AGCGCTGACGACGAGTGGCGGCTGACGATCATCAGCAGC 1080

RESULT 35
US-10-156-761-6327
Sequence 6327, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMIYA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
PRIOR FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 6327
LENGTH: 1581

```

; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1581)
US-10-156-761-6327

Query Match
Best Local Similarity 59.1%; Score 38; DB 15; Length 1581;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 42 CCGAGCTGTCATCTCGTCATCTCGATCGAGTCGCGCGCCGACCTCGACGATGAGCGAGA 101
Db 308 CCGAGTACGTACGACGCGCCCTCGACGCGGCGGTGACCGAGCGCCGTCGAAACGCGAGG 367
Oy 102 TGACACAGCTCCGCGCCGACCTCGACGATGAGCGAGATGACCACTCCGG 151
Db 368 TCGTCGCTCCGTCGTCGACGCGCCGACGAGCCGCGGAACTGCTCGGG 417

RESULT 36
US-10-156-761-6327/c
; Sequence 6327, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 6327
; LENGTH: 1581
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1581)
US-10-156-761-6327

Query Match
Best Local Similarity 59.1%; Score 38; DB 15; Length 1581;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 4 CCGAGCTGTCATCTCGTCATCTCGATCGAGTCGCGCGCCGACCTCGATCTCGTCAT 63
Db 417 CCGAGGAGTTCGCGCGGCTCGTCGCGGCTCGACGATCGGAGCGACGACCTCGGCTT 358
Oy 64 CGTGAAGTCGCGCGCGCGCGACCTCGACGATGAGCGAGATGACCACTCCG 113
Db 357 CGAGCGGCTCGTCGTCGTCGCGCGGCTCGAGCGGCGGCTTGACGTACTCGG 308

RESULT 37
US-10-156-761-1
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match
Best Local Similarity 59.1%; Score 38; DB 15; Length 9025608;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 4 CCGAGCTGTCATCTCGTCATCTCGATCGAGTCGCGCGCCGACCTCGATCTCGTCAT 63
Db 7618860 CCGAGAGTTCGCGCGGCTCGTCGCGGCTCGACGATGAGCGAGCGACGACTCGCGGTT 7618801
```

```

; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match
Best Local Similarity 59.1%; Score 38; DB 15; Length 9025608;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 42 CCGAGCTGTCATCTCGTCATCTCGATCGAGTCGCGCGCCGACCTCGACGATGAGCGAGA 101
Db 7618751 CCGAGTACGTACGACGCGCCCTCGACGCGGCGGTGACCGAGCGCCCTCGAACCGCGAGG 7618810
Oy 102 TGACACAGCTCCGCGCCGACCTCGACGATGAGCGAGATGACCACTCCGG 151
Db 7618811 TCGTCGCTCCGTCGTCGACGCGCCGACGAGCCGCGGAACTGCTCGGG 7618860
```

```

US-10-156-761-1/c
; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1

Query Match
Best Local Similarity 59.1%; Score 38; DB 15; Length 9025608;
Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

Oy 4 CCGAGCTGTCATCTCGTCATCTCGATCGAGTCGCGCGCCGACCTCGATCTCGTCAT 63
Db 7618860 CCGAGAGTTCGCGCGGCTCGTCGCGGCTCGACGATGAGCGAGCGACGACTCGCGGTT 7618801
```


Qy 64 CGTGCAGTCGGCGCCGCGCACTCGACGATGAGCGAGTACCACTCCG 113
Db 7618800 CGACGGGCGCTGCTCAACGCCCGGTGACGGCGCCCTTGAAGTACTCG 7618751

RESULT 39

US-10-437-963-43250
; Sequence 43250, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 43250
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46425C.1
US-10-437-963-43250

Query Match 24.0%; Score 37; DB 18; Length 1821;
Best Local Similarity 53.0%; Pred. No. 0.058;
Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATGCTGAGTGGGCGGAGCTGTCATCTCGCT 60
Db 828 CGTCCGAGCGGCTCTTCTCTGCGCGGCGCTGCTGCTGCTGCGCCACTGCT 887
Qy 61 CATGTCGAGTGGCGGCGCGCGCACTCGACGATGAGCGAGTACCACTCCGCGCG 120
Db 888 GCTGCGCGCGCGCGCGCGCATGCGCCGTCCTCGAGAGCGTCTCTGCGCGCGT 947
Qy 121 ACTGACGATGAGCGAGTACCACTCC 149
Db 948 CTCGACGCGCGGAGCGAGCGTGCAGCGCC 976

RESULT 40

US-10-437-963-43250/C
; Sequence 43250, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 43250
; LENGTH: 1821
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_46425C.1
US-10-437-963-43250

Query Match 24.0%; Score 37; DB 18; Length 1821;
Best Local Similarity 53.0%; Pred. No. 0.058;
Matches 79; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

Qy 6 GGAGCTGATCATCTCGCTCATGCTGAGTGGGCGGCGGAGCTGTCATCTCGCTCATCG 65
Db 976 GCGCTGACGCTCGCTCTCGCGCTGAGAGCGCGGCGAGAGAGAGAGAGAGAG 917
Qy 66 TCGAGTGGGCGCGCGCGCACTCGACGATGAGCGAGTACCACTCCGCGCGACTCG 125
Db 916 GCAGGCGGATGCGCGCGCGCGCGAGCAGGAGTGGCGGCGAGCGAGCGAGCG 857
Qy 126 ACGATGACGAGATGACCACTCCGCGCG 154
Db 856 CCGCGCAGAGAGAGAGCGCGCTCGGAGCG 828

RESULT 41

US-10-437-963-51952
; Sequence 51952, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 51952
; LENGTH: 742
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_54296C.1
US-10-437-963-51952

Query Match 23.6%; Score 36.4; DB 18; Length 742;
Best Local Similarity 58.2%; Pred. No. 0.093;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 42 CGGAGCTGTCATCTCGCTCATGCTGAGTGGGCGCGCGCACTCGACGATGAGCGAGA 101
Db 173 CCGCGTTCGCGTACCCCGGTGTCGTCCTCGCGCGCGCTCGATGAGAGCAACA 232
Qy 102 TGACCACTCCGCGCGCGCACTCGACGATGAGCGAGTACCACTCCGCG 151
Db 233 GCTTGGGTGAGTCTCGCGGTTCGCGCGCGCGCGCGAGCAGCACTCCGCG 282

RESULT 42

US-10-437-963-51952/C
; Sequence 51952, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

Query Match	23.4%	Score 36;	DB 18;	Length 816;
Best Local Similarity	55.6%	Pred. No. 0.12;		
Matches 69;	Conservative 0;	Mismatches 55;	Indels 0;	Gaps 0;

```

Oy      31  AAGTGGGCGCGGAGCTGTGATCTGGCTCATGTCGATGGCGGCGCGGACTCGAC  90
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      418  GAGCGGAGCAGGATTCGGAGCGGCTTCACCAAGACTTGTCGGCGCGCGCGCGCAC  477
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      91  GATGACGAGATGACCAAGCTCGGCGCGCGGACTCGACGATGAGCGGATGACCAAGCTCGG  150
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      478  CACCAACCAACCAACCAAGACCGCGCGCGCGCGCACTCGGACCACTACTGAGCCCC  537
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Oy      151  GCGG  154
          ||| |||
Db      538  GCGG  541

```

Search completed: April 9, 2005, 01:03:46
Job time : 528 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 21:38:34 ; Search time 434 Seconds
(without alignments)
2100.553 Million cell updates/sec

Title: US-09-887-194A-13

Perfect score: 154
Sequence: 1 cggccggagctgctcatctc.....gagatgacacagctccgagcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : N_Geneseq_16Dec04:*

1: geneseq1980s:*
2: geneseq1990s:*
3: geneseq2000s:*
4: geneseq2001as:*
5: geneseq2001bs:*
6: geneseq2002as:*
7: geneseq2002bs:*
8: geneseq2003as:*
9: geneseq2003bs:*
10: geneseq2003cs:*
11: geneseq2003ds:*
12: geneseq2004as:*
13: geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	154	100.0	154	6	AAD29231 Plasmids
2	154	100.0	154	6	AAD29231 Plasmids
3	154	100.0	154	6	AAD32908 Plasmids
4	154	100.0	154	6	AAD32908 Plasmids
5	154	100.0	154	12	ADQ07968 Seed spec
6	154	100.0	154	12	ADQ07968 Seed spec
7	154	100.0	7701	12	ADP89887 Seed-spec
8	154	100.0	7701	12	ADP89887 Seed-spec
9	154	100.0	7701	12	ADP89887 Seed-spec
10	154	100.0	7701	12	ADP89887 Seed-spec
11	154	100.0	7701	12	ADP89887 Seed-spec
12	154	100.0	7701	12	ADQ07962 Seed spec
13	154	100.0	7701	12	ADQ07962 Seed spec
14	154	100.0	7701	12	ADQ07962 Seed spec
15	154	100.0	7701	12	ADQ07962 Seed spec
16	154	100.0	7701	12	ADQ07962 Seed spec
17	154	100.0	7701	12	ADQ07962 Seed spec
18	154	100.0	7701	12	ADQ07962 Seed spec
19	154	100.0	7701	12	ADQ07962 Seed spec
20	154	100.0	7701	12	ADQ07962 Seed spec

21	80	51.9	80	6	AAD29230 Plasmids
22	80	51.9	80	6	AAD29230 Plasmids
23	80	51.9	80	6	AAD32907 Plasmids
24	80	51.9	80	6	AAD32907 Plasmids
25	80	51.9	92	6	ABK10712 Artificialia
26	80	51.9	92	6	ABK10712 Artificialia
27	80	51.9	92	6	ABK10712 Artificialia
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29	80	51.9	92	6	ABK10712 Artificialia
30	80	51.9	92	6	ABK10712 Artificialia
31	80	51.9	92	6	ABK10712 Artificialia
32	80	51.9	92	6	ABK10712 Artificialia
33	80	51.9	92	6	ABK10712 Artificialia
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37	80	51.9	92	6	ABK10712 Artificialia
38	80	51.9	92	6	ABK10712 Artificialia
39	80	51.9	92	6	ABK10712 Artificialia
40	80	51.9	92	6	ABK10712 Artificialia
41	80	51.9	92	6	ABK10712 Artificialia
42	80	51.9	92	6	ABK10712 Artificialia
43	80	51.9	92	6	ABK10712 Artificialia
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60	80	51.9	92	6	ABK10712 Artificialia
61	80	51.9	92	6	ABK10712 Artificialia
62	80	51.9	92	6	ABK10712 Artificialia
63	80	51.9	92	6	ABK10712 Artificialia
64	80	51.9	92	6	ABK10712 Artificialia
65	80	51.9	92	6	ABK10712 Artificialia
66	80	51.9	92	6	ABK10712 Artificialia
67	80	51.9	92	6	ABK10712 Artificialia
68	80	51.9	92	6	ABK10712 Artificialia
69	80	51.9	92	6	ABK10712 Artificialia
70	80	51.9	92	6	ABK10712 Artificialia
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78	80	51.9	92	6	ABK10712 Artificialia
79	80	51.9	92	6	ABK10712 Artificialia
80	80	51.9	92	6	ABK10712 Artificialia
81	80	51.9	92	6	ABK10712 Artificialia
82	80	51.9	92	6	ABK10712 Artificialia
83	80	51.9	92	6	ABK10712 Artificialia
84	80	51.9	92	6	ABK10712 Artificialia
85	80	51.9	92	6	ABK10712 Artificialia
86	80	51.9	92	6	ABK10712 Artificialia
87	80	51.9	92	6	ABK10712 Artificialia
88	80	51.9	92	6	ABK10712 Artificialia
89	80	51.9	92	6	ABK10712 Artificialia
90	80	51.9	92	6	ABK10712 Artificialia
91	80	51.9	92	6	ABK10712 Artificialia
92	80	51.9	92	6	ABK10712 Artificialia
93	80	51.9	92	6	ABK10712 Artificialia

94	32.4	21.0	2034	12	ADJ44932	Adj44932 Plant cDN
95	32.4	21.0	2237	2	ABO89779	ABO89779 Cocranspo
96	32.4	21.0	2237	2	ABO89779	ABO89779 Cocranspo
97	32.4	21.0	135538	10	ABX34289	ABx34289 S. atrocol
98	32.4	21.0	135538	10	ABX34289	ABx34289 S. atrocol
99	32.2	20.9	441	12	ADJ44648	Adj44648 Plant cDN
100	32.2	20.9	441	12	ADJ44648	Adj44648 Plant cDN

CC	RESULT 1
XX	AAD29231
XX	AAD29231 standard; DNA; 154 BP.
AC	AAD29231;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.
XX	
KM	Recombinant construct; gene expression; plasmid pKS133; ds.
XX	
OS	Unidentified.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	7..36
FT	/tag= a
FT	/product= "ELVISLIVES protein"
FT	44..74
FT	/tag= b
FT	/product= "ELVISLIVES protein"
FT	complement(82..111)
FT	/tag= c
FT	/product= "ELVISLIVES protein"
FT	complement(119..148)
FT	/tag= d
FT	/product= "ELVISLIVES protein"
XX	
PN	WO200200904-A2.
XX	
PD	03-JAN-2002.
XX	
PF	22-JUN-2001; 2001WO-US019962.
XX	
PR	23-JUN-2000; 2000US-0213961P.
XX	
PA	(DUBO) DU PONT DE NEMOURS & CO E I.
XX	
PA	(PION-) PIONEER HI-BRED INT INC.
XX	
PI	Glaesman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca XL;
PI	Nichols SE;
XX	
DR	WPI; 2002-139927/18.
XX	
DR	P-PSDB; AAE18333.
XX	
PT	New recombinant construct having a promoter operably linked to a DNA
PT	sequence which when expressed produces an RNA having homology to a target
PT	mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT	gene expression.
XX	
PS	Claim 45; Page 37; 77pp; English.
XX	
XX	The present invention relates to a new recombinant construct. The
CC	construct comprises a promoter operably linked to a DNA sequence which
CC	when expressed by a host produces an RNA having homology to at least one
CC	target mRNA expressed by the host and complementary RNA regions. The
CC	recombinant construct is useful for reducing the expression of a target
CC	mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC	recombinant constructs are also used in reducing expression of a target
CC	mRNA or any similar endogenous mRNA. The sequences and their reverse
CC	complements can be used to reduce the expression of any endogenous

CC	genomic sequence that shares substantial similarity to nucleic acid
CC	fragment which is in proximity to the DNA or RNA sequence derived from
CC	it. The present sequence is 2X ELVISIVUS complementary repeat region DNA
CC	found in plasmid pK313 used in the exemplification of the invention
XX	
SQ	Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match	100.0%; Score 154; DB 6; Length 154;
Best Local Similarity	100.0%; Pred. NO. 2.7e-28;
Matches 154;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 CGGCCGAGCTGTATCTCGCTCATCGTCGAGTGGCGCGCGAGCTGTGCATCTCGCT 60
Db	1 CGGCCGAGCTGTGCATCTCGCTCATCGTCGAGTGGCGCGCGAGCTGTGCATCTCGCT 60
QY	61 CATGTCGAGTCGGCGCGCCCGCACTCGACGATGAGCGAGATGAACAAGCTCCGCGCGC 120
Db	61 CATGTCGAGTCGGCGCGCCCGCACTCGACGATGAGCGAGATGAACAAGCTCCGCGCGC 120
QY	121 ACTGAGCATGAGCGAGATGACCAAGCTCCGCGCG 154
Db	121 ACTGAGCATGAGCGAGATGACCAAGCTCCGCGCG 154

ID	AAID29231/C	standard; DNA; 154 BP.
XX	AAID29231;	
XX	07-MAY-2002	(first entry)
XX	Plasmids pKS133 2X ELVISLIVES complementary repeat DNA.	
XX	Recombinant construct; gene expression; plasmid pKS133; ds.	
XX	Unidentified.	
XX	Key	Location/Qualifiers
XX	CDS	7..36
XX		/*tag= a
XX		/product= "ELVISLIVES protein"
XX		44..74
XX	CDS	/*tag= b
XX		/product= "ELVISLIVES protein"
XX		complement(82..111)
XX	CDS	/*tag= c
XX		/product= "ELVISLIVES protein"
XX		complement(119..148)
XX	CDS	/*tag= d
XX		/product= "ELVISLIVES protein"
XX	WO200200904-A2.	
XX	03-JAN-2002.	
XX	22-JUN-2001; 2001WO-US019962.	
XX	23-JUN-2000; 2000US-0213961P.	
XX	(DUPO) DU PONT DE NEMOURS & CO E I.	
XX	(PION-) PIONEER HI-BRED INT INC.	
XX	Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,	
XX	Nichols SE;	
XX	WPI; 2002-139927/18.	
XX	P-PSDB; AAE18353.	
XX	New recombinant construct having a promoter operably linked to a DNA	
XX	PT sequence which when expressed produces an RNA having homology to a target	
XX	PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing	
XX	PT gene expression.	

XX Claim 45; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The

CC construct comprises a promoter operably linked to a DNA sequence which

CC when expressed by a host produces an RNA having homology to at least one

CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target

CC mRNA or any similar endogenous mRNA. The RNAs expressed from the

CC recombinant constructs are also used in reducing expression of a target

CC mRNA or any similar endogenous mRNA. The sequences and their reverse

CC complements can be used to reduce the expression of any endogenous

CC genomic sequence that shares substantial similarity to nucleic acid

CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2X ELVISLIVES complementary repeat region DNA

CC found in plasmid pKS133 used in the exemplification of the invention

XX

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60

DB 154 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 95

QY 61 CATGTCGATGTCGGCGCGCGCGGAGTCGAGATGAGCGAGTCCGCGCGCG 120

DB 94 CATGTCGATGTCGGCGCGCGCGGAGTCGAGATGAGCGAGTCCGCGCGCG 35

QY 121 ACTGACGATGAGGAGATGACCAAGCTCCGCGCG 154

DB 34 ACTGACGATGAGGAGATGACCAAGCTCCGCGCG 1

RESULT 3

AAID32908

AC AAD32908; standard; DNA; 154 BP.

XX

DT 01-JUL-2002 (first entry)

XX

DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

XX

KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KW ds.

XX

OS Unidentified.

XX

XX Location/Qualifiers

XX Key 7..36

XX CDS /*tag= a

FT /product= "ELVISLIVES protein"

FT 44..74

FT /*tag= b

FT /product= "ELVISLIVES protein"

FT complement (82..111)

FT /*tag= c

FT /product= "ELVISLIVES protein"

FT complement (119..148)

FT /*tag= d

FT /product= "ELVISLIVES protein"

XX

XX WO200216565-A2.

XX

XX 28-FEB-2002.

XX

XX 22-AUG-2001; 2001WO-USO26246.

XX

XX 22-AUG-2000; 2000US-0226996P.

XX (DUPO) DU PONT DE NEMOURS & CO E. I.

XX

PI Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;

XX

DR WPI; 2002-269353/31.

XX

DR P-PSDB; AAE20554.

XX

PT New delta-9 fatty acid desaturase polypeptides and polynucleotides,

PT useful in creating transgenic plants having altered levels of mono-, poly

PT - and unsaturated fatty acids and in increasing the unsaturation levels

PT in cellular lipids.

XX

XX Example 9; Page 43; 77pp; English.

XX

CC The present invention relates to diverged delta-9 fatty acid desaturase

CC proteins and polynucleotides encoding such proteins. The nucleic acid

CC sequences may be used to increase the level of unsaturation in cellular

CC lipids, including oil, in tissues when the enzyme is absent or rate-

CC limiting, to isolate cDNAs and genes encoding homologous proteins from

CC the same or other plant species and to create transgenic plants in which

CC the polypeptides are present at higher or lower levels than normal or in

CC cell types or developmental stages in which they are not normally found,

CC thus altering the level of mono-, poly- and unsaturated fatty acids in

CC those cells. They are useful as probes for genetic and physical gene

CC mapping and as markers, e.g. restriction fragment length polymorphism

CC (RFLP) markers. The peptides can be used to immunise animals to produce

CC antibodies specific for the peptides and proteins. The present sequence

CC is 1X ELVISLIVES complementary repeat region DNA found in plasmid pKS133

CC This sequence is used in the exemplification of the invention for the

CC suppression of Pad2 in soybean

XX

SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;

Query Match 100.0%; Score 154; DB 6; Length 154;

Best Local Similarity 100.0%; Pred. No. 2.7e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60

DB 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60

QY 61 CATGTCGATGTCGGCGCGCGCGGAGTCGAGATGAGCGAGTCCGCGCGCG 120

DB 61 CATGTCGATGTCGGCGCGCGCGGAGTCGAGATGAGCGAGTCCGCGCGCG 120

QY 121 ACTGACGATGAGGAGATGACCAAGCTCCGCGCG 154

DB 121 ACTGACGATGAGGAGATGACCAAGCTCCGCGCG 154

RESULT 4

AAID32908/c

ID AAD32908 standard; DNA; 154 BP.

XX

AC AAD32908;

XX

DT 01-JUL-2002 (first entry)

XX

DE Plasmid pKS133 2X ELVISLIVES complementary repeat DNA.

XX

KW Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;

KW oil; transgenic plant; gene mapping; immunisation; plasmid pKS133; gene;

KW ds.

XX

OS Unidentified.

XX

XX Location/Qualifiers

XX Key 7..36

XX CDS /*tag= a

FT /product= "ELVISLIVES protein"

FT 44..74

FT /*tag= b

Qy 61 CATGCTGAGTGGGCGGCGGCGACTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
Dy 61 CATGCTGAGTGGGCGGCGGCGGCGACTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
Qy 121 ACTGACGATGAGCGAGATGACCACTCCGGCGCG 154
Dy 121 ACTGACGATGAGCGAGATGACCACTCCGGCGCG 154

RESULT 6
AD007968/C
ID AD007968 standard; DNA; 154 BP.
AC AD007968;
XX
XX 23-SEP-2004 (first entry)
Dy
XX Seed specific gene silencing vector pKS151, stem loop region.
XX
XX pKS151, seed specific promoter; gene silencing; chalcone reductase;
KM transgenic; liquiritigenin-derived isoflavone; isoflavonoid;
KM food product; snack food product; baked good product; fried food product;
KM health food product; infant formula; beverage; nutritional supplement;
KM dairy product; pet food product; animal feed; ss.
XX
XX Synthetic.
OS
FH Key Location/Qualifiers
FT stem_loop 1..154
FT /*tag= a

US2004128714-A1.
XX
XX 01-JUL-2004.
XX
XX 11-DEC-2003; 2003US-00734947.
XX
XX 13-DEC-2002; 2002US-0433433P.
XX
XX (MCGO/) MCGONIGLE B.
XX
XX MCGONIGLE B;
PI
XX WPI: 2004-533136/51.
XX
XX Decreasing ratio of liquiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).
XX
XX Example 7; SEQ ID NO 7; 25pp; English.

The invention relates to decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavonoid-producing plant comprising transforming a plant cell with a recombinant construct comprising a promoter operably linked to a nucleic acid sequence of at least 200 nucleotides having at least 75% sequence identity to AD007965 (a soybean chalcone reductase cDNA). Also included are an isoflavonoid-producing plant made by the method above, seeds or plant parts of the plant, an isoflavonoid-containing protein product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels obtained from the seeds or plant parts, a food (or a nutritional supplement, a food bar, or a beverage) which has incorporated the isoflavonoid-containing product, and a method of producing an isoflavonoid-containing product having a reduced ratio of liquiritigenin-derived isoflavones relative to the total isoflavone levels. The recombinant construct comprises a stem-loop structure. The nucleic acid sequence forms a loop in the stem-loop structure and the stem comprises a sequence of AD007968. The promoter is a seed-specific promoter. The method is useful for decreasing the ratio of liquiritigenin-derived isoflavones relative to the total isoflavones in an isoflavone-producing plant. The methods and recombinant construct are useful in producing an isoflavonoid-containing product which is incorporated in

CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the single stranded version of the stem loop region from
CC plasmid pKS151.
XX
SQ Sequence 154 BP; 24 A; 53 C; 53 G; 24 T; 0 U; 0 Other;
Query Match 100.0%; Score 154; DB 12; Length 154;
Best Local Similarity 100.0%; Pred. No. 2,7e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGATCATCTCGCTCATCTCGAGTCGGGCGGAGCTGATCTGCT 60
Dy 154 CGGCGGAGCTGATCATCTCGCTCATCTCGAGTCGGGCGGAGCTGATCTGCT 95
Qy 61 CATGCTGAGTGGGCGGCGGCGGCGACTCGACGATGAGCGAGATGACCACTCCGGCGCG 120
Dy 94 CATGCTGAGTGGGCGGCGGCGGCGGCGACTCGACGATGAGCGAGATGACCACTCCGGCGCG 35
Qy 121 ACTGACGATGAGCGAGATGACCACTCCGGCGCG 154
Dy 34 ACTGACGATGAGCGAGATGACCACTCCGGCGCG 1

RESULT 7
ADF89887
ID ADF89887 standard; DNA; 7701 BP.
AC ADF89887;
XX
XX 26-FEB-2004 (first entry)
Dy
XX
XX Seed-specific expression vector pKS151 nucleotide sequence.
DE
XX
XX Oxidogualene cyclase; triterpene; plant protectant; industrial product;
KM plant; soybean; beta-amyrin synthase; ds.
KM
XX
XX Synthetic.
OS
XX
XX WO2003095615-A2.
XX
XX 20-NOV-2003.
XX
XX 05-MAY-2003; 2003WO-US014218.
XX
XX 09-MAY-2002; 2002US-0379361P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX MCGONIGLE B, Maxwell CA, Hession MO;
PI
XX WPI: 2004-012098/01.
XX
XX New transgenic plants comprising recombinant DNA molecules encoding
PT oxidogualene cyclase to lower triterpene level, used as feeds, foods,
PT beverages and industrial products like agricultural adjuvants or concrete
PT supplies.
XX
XX Example 1; SEQ ID NO 9; 39pp; English.

The invention relates to a plant comprising at least one recombinant DNA molecule comprising a promoter operably linked to at least a portion of at least one oxidogualene cyclase gene, the molecule sufficient to suppress the production of a triterpene or any of its progeny, where the progeny comprise the molecule. The oxidogualene cyclase gene catalyzes the cyclization of 2,3-oxidogualene to form a triterpene, e.g. beta-amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultifloranol or any combination. The plants are useful in generating products which may be used as feeds, foods, beverages and industrial products like agricultural adjuvants, concrete supplies, dielectric fluids, dust suppressants, fuel additives, hydraulic fluids, industrial cleaners, industrial lubricants, metalworking fluids, odor reduction, paint

CC stripers, printing inks, printing supplies or saw guide oils. Saponins
CC may play a defense role against pathogens in plant tissues. The present
CC sequence represents the nucleotide sequence of a seed-specific expression
CC vector pKS151.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGCTCATCTGCTCATCTGAGTCGGCGCGGAGCTGCTCATCTGCT 60
Db CGGCCGAGCTGCTCATCTGCTCATCTGAGTCGGCGCGGAGCTGCTCATCTGCT 5510
QY 61 CATGTCGAGTCGGCGCGCGCGGAGCTGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 120
Db CATGTCGAGTCGGCGCGCGCGGAGCTGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 5570
QY 121 ACTGACGATGAGCGAGATGACCACTCCGCGC 154
Db ACTGACGATGAGCGAGATGACCACTCCGCGC 5571

RESULT 8

ADP8987/C
ID ADP8987 standard; DNA; 7701 BP.

XX
AC ADP8987;

XX
DT 26-FEB-2004 (first entry)

XX
DE Seed-specific expression vector pKS151 nucleotide sequence.

XX
KM Oxidogualene cyclase; triterpene; plant protectant; industrial product;
KM plant; soybean; beta-amyrin synthase; ds.

XX
OS Synthetic.

XX
PN WO2003095615-A2.

XX
PD 20-NOV-2003.

XX
PF 05-MAY-2003; 2003WO-US014218.

XX
PR 09-MAY-2002; 2002US-0379361P.

XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX
PI Mcgonigle B, Maxwell CA, Hession AO;

XX
DR WPI; 2004-012098/O1.

XX
PT New transgenic plants comprising recombinant DNA molecules encoding
PT oxidogualene cyclase to lower triterpene level, used as feeds, foods,
PT beverages and industrial products like agricultural adjuvants or concrete
PT supplies.

XX
PS Example 1; SEQ ID NO 9; 39pp; English.

XX
CC The invention relates to a plant comprising at least one recombinant DNA
CC molecule comprising a promoter operably linked to at least a portion of
CC at least one oxidogualene cyclase gene, the molecule sufficient to
CC suppress the production of a triterpene or any of its progeny, where the
CC progeny comprise the molecule. The oxidogualene cyclase gene catalyzes
CC the cyclization of 2,3-oxidosqualene to form a triterpene, e.g. beta-
CC amyrin, lanosterol, lupeol, cycloartenol, alpha-amyrin, isomultifloranol
CC or any combination. The plants are useful in generating products which
CC may be used as feeds, foods, beverages and industrial products like
CC agricultural adjuvants, concrete supplies, dielectric fluids, dust
CC suppressants, fuel additives, hydraulic fluids, industrial cleaners,
CC industrial lubricants, metalworking fluids, odor reduction, paint
CC stripers, printing inks, printing supplies or saw guide oils. Saponins

CC may play a defense role against pathogens in plant tissues. The present
CC sequence represents the nucleotide sequence of a seed-specific expression
CC vector pKS151.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGCTCATCTGCTCATCTGAGTCGGCGCGGAGCTGCTCATCTGCT 60
Db CGGCCGAGCTGCTCATCTGCTCATCTGAGTCGGCGCGGAGCTGCTCATCTGCT 5545
QY 61 CATGTCGAGTCGGCGCGCGCGGAGCTGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 120
Db CATGTCGAGTCGGCGCGCGCGGAGCTGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 5485
QY 121 ACTGACGATGAGCGAGATGACCACTCCGCGC 154
Db ACTGACGATGAGCGAGATGACCACTCCGCGC 5484

RESULT 9

ADP67892
ID ADP67892 standard; DNA; 7701 BP.

XX
AC ADP67892;

XX
DT 11-MAR-2004 (first entry)

XX
DE Seed-specific expression vector pKS151 #SEQ ID 1.

XX
KM Isoflavonoid; transgenic plant; flavanone 3-hydroxylase; ds.

XX
OS Synthetic.

XX
PN WO2003106633-A2.

XX
PD 24-DEC-2003.

XX
PF 12-JUN-2003; 2003WO-US018663.

XX
PR 13-JUN-2002; 2002US-0388280P.

XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX
PI Mcgonigle B, Odell JT;

XX
DR WPI; 2004-062526/O6.

XX
PT Increasing isoflavonoid production in an isoflavonoid-producing plant.
PT comprises transforming a plant with recombinant DNA constructs, growing
PT the transformed plant, and evaluating increased quantity of isoflavonoid.

XX
PS Example 1; SEQ ID NO 1; 55pp; English.

XX
CC The invention relates to a method for increasing isoflavonoid production
CC in a plant, by transforming the plant with a recombinant DNA construct
CC having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone
CC 3-hydroxylase, and second recombinant DNA construct having a PN encoding
CC C1 myb and a R myc-type transcription factor, growing the transformed
CC plant, and evaluating the quantity of isoflavonoid from the plant. The
CC method of the invention is useful for increasing isoflavonoid production
CC in an isoflavonoid-producing plant. The current sequence represents the
CC seed-specific expression vector pKS151, into which a polynucleotide
CC encoding a portion of soybean flavanone 3-hydroxylase was inserted in an
CC example from the invention, for the transformation of Glycine max.

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGGTCATCTGCTCATCTGTCAGTCGGGCGGAGGTCATCTGCT 60
Db 5451 CGGCGGAGGTCATCTGCTCATCTGTCAGTCGGGCGGAGGTCATCTGCT 5510

Qy 61 CATGTCGAGTCGGCGCGCGGCGGACTCGACGATGAGGAGATGACCAAGCTCCGGCGCG 120
Db 5511 CATGTCGAGTCGGCGCGCGGCGGACTCGACGATGAGGAGATGACCAAGCTCCGGCGCG 5570

Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCGCG 154
Db 5571 ACTGACGATGAGGAGATGACCAAGCTCCGGCGCG 5604

RESULT 10
ADF67892/c
ID ADF67892 standard; DNA; 7701 BP.
XX
AC ADF67892;
XX
DT 11-MAR-2004 (first entry)
XX
DE Seed-specific expression vector PKS151 #SEQ ID 1.
XX
KW Isoflavonoid; transgenic plant; flavanone 3-hydroxylase; ds.
XX
OS Synthetic.
XX
PN WO2003106633-A2.
XX
PD 24-DEC-2003.
XX
PF 12-JUN-2003; 2003WO-US018663.
XX
PR 13-JUN-2002; 2002US-0388280P.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PI Mgonigle B, Odell JT;
XX
DR WPI; 2004-062526/06.
XX
PT Increasing isoflavonoid production in an isoflavonoid-producing plant.
PT comprises transforming a plant with recombinant DNA constructs, growing
PT the transformed plant, and evaluating increased quantity of isoflavonoid.
XX
XX Example 1; SEQ ID NO 1; 55pp; English.
XX
CC The invention relates to a method for increasing isoflavonoid production
CC in a plant, by transforming the plant with a recombinant DNA construct
CC having a polynucleotide (PN) e.g., a PN encoding all or part of flavanone
CC 3-hydroxylase, and second recombinant DNA construct having a PN encoding
CC C1 myb and a R myc-type transcription factor, growing the transformed
CC plant, and evaluating the quantity of isoflavonoid from the plant. The
CC method of the invention is useful for increasing isoflavonoid production
CC in an isoflavonoid-producing plant. The current sequence represents the
CC seed-specific expression vector PKS151, into which a polynucleotide
CC encoding a portion of soybean flavanone 3-hydroxylase was inserted in an
CC example from the invention, for the transformation of Glycine max.
XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGGTCATCTGCTCATCTGTCAGTCGGGCGGAGGTCATCTGCT 60
Db 5604 CGGCGGAGGTCATCTGCTCATCTGTCAGTCGGGCGGAGGTCATCTGCT 5545

Qy 61 CATGTCGAGTCGGCGCGCGGCGGACTCGACGATGAGGAGATGACCAAGCTCCGGCGCG 120
Db 5571 CATGTCGAGTCGGCGCGCGGCGGACTCGACGATGAGGAGATGACCAAGCTCCGGCGCG 5570

Db 5544 CATGTCGAGTCGGCGCGCGGCGGACTCGACGATGAGGAGATGACCAAGCTCCGGCGCG 5485
Qy 121 ACTGACGATGAGGAGATGACCAAGCTCCGGCGCG 154
Db 5484 ACTGACGATGAGGAGATGACCAAGCTCCGGCGCG 5451

RESULT 11
ADQ07962
ID ADQ07962 standard; DNA; 7701 BP.
XX
AC ADQ07962;
XX
DT 23-SEP-2004 (first entry)
XX
DE Seed specific gene silencing vector PKS151.
XX
KW PKS151; seed specific promoter; gene silencing; chalcone reductase;
KW transgenic; liquiritigenin-derived isoflavone; plant; soybean;
KW isoflavonoid; food product; snack food product; baked good product;
KW fried food product; health food product; infant formula; beverage;
KW nutritional supplement; dairy product; pet food product; animal feed; ds.
XX
OS Glycine max.
OS Escherichia coli.
OS Cauliflower mosaic virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 5457..5486
FT /tag= a
FT /partial
FT /note= "No start or stop codon shown"
FT /product= "ELVITLIVES peptide"

US2004128714-A1.
01-JUL-2004.
11-DEC-2003; 2003US-00734947.
13-DEC-2002; 2002US-0433433P.
(MCGO/) MCGONIGLE B.
Mgonigle B;
WPI; 2004-533136/51.
P-PSDB; ADQ07969.

XX
XX Example 1; SEQ ID NO 1; 25pp; English.
XX
CC The invention relates to decreasing the ratio of liquiritigenin-derived
CC isoflavones relative to the total isoflavones in an isoflavonoid-
CC producing plant comprising transforming a plant cell with a recombinant
CC construct comprising a promoter operably linked to a nucleic acid
CC sequence of at least 200 nucleotides having at least 75% sequence
CC identity to ADQ07965 (a soybean chalcone reductase cDNA). Also included
CC are an isoflavonoid-producing plant made by the method above, seeds or
CC plant parts of the plant, an isoflavonoid-containing protein product
CC having a reduced ratio of liquiritigenin-derived isoflavones relative to
CC the total isoflavone levels obtained from the seeds or plant parts, a
CC food (or a nutritional supplement, a food bar, or a beverage) which has
CC incorporated the isoflavonoid-containing product, and a method of
CC producing an isoflavonoid-containing product having a reduced ratio of
CC liquiritigenin-derived isoflavones relative to the total isoflavone
CC levels. The recombinant construct comprises a stem-loop structure. The
CC nucleic acid sequence forms a loop in the stem-loop structure and the

CC stem comprises a sequence of AD007968). The promoter is a seed-specific
CC promoter. The method is useful for decreasing the ratio of liguiritigenin
CC-derived isoflavones relative to the total isoflavones in an isoflavone-
CC producing plant. The methods and recombinant construct are useful in
CC producing an isoflavonoid-containing product which is incorporated in
CC cereal food product, snack food product, baked good product, fried food
CC product, health food product, infant formula, beverage, nutritional
CC supplement, dairy product, pet food product, or animal feed. The present
CC sequence is the seed specific gene silencing vector pKS151, into which
CC the soybean cDNA is cloned (into the NotI site flanked by the stem
CC regions of AD007968).

XX Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;
SQ

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 5451 CGGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTGCT 5510
QY 61 CATGCTGAGTCGGCGCGCGCGGAGTCGAGATGACCAAGCTCCGGCGCGG 120
Db 5511 CATGCTGAGTCGGCGCGCGCGGAGTCGAGATGACCAAGCTCCGGCGCGG 5570
QY 121 ACTGACGATGAGCGAGATGACCAAGCTCCGGCGG 154
Db 5571 ACTGACGATGAGCGAGATGACCAAGCTCCGGCGG 5604

RESULT 12
AD007962/c
ID AD007962 standard; DNA; 7701 BP.
XX
AC AD007962;
XX
DT 23-SEP-2004 (first entry)
XX
DE Seed specific gene silencing vector pKS151.
XX
KW pKS151; seed specific promoter; gene silencing; chalcone reductase;
KW transgenic; liguiritigenin-derived isoflavone; plant; soybean;
KW isoflavonoid; food product; snack food product; baked good product;
KW fried food product; health food product; infant formula; beverage;
KW nutritional supplement; dairy product; pet food product; animal feed; ds.
XX
OS Glycine max.
OS Escherichia coli.
OS Cauliflower mosaic virus.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 5457..5486
FT /tag= a
FT /partial
FT /note= "No start or stop codon shown"
FT /product= "ELVISLIVES peptide"
XX
XX US2004128714-A1.
XX
XX
XX PD 01-JUL-2004.
XX
XX PF 11-DEC-2003; 2003US-00734947.
XX
XX PR 13-DEC-2002; 2002US-0433433P.
XX
XX PA (MCGO/) MCGONIGLE B.
XX
XX PI Mgonigle B;
XX
XX WPI; 2004-533136/51.
XX
XX P-PSDB; AD007969.
DR

XX
PT Decreasing ratio of liguiritigenin-derived isoflavones relative to total
PT isoflavones in a plant comprises transforming plant cell with nucleic
PT acid sequence showing homology to sequence encoding chalcone reductase
PT (deoxychalcone synthase).

PS Example 1; SEQ ID NO 1; 25pp; English.

XX
XX The invention relates to decreasing the ratio of liguiritigenin-derived
XX isoflavones relative to the total isoflavones in an isoflavonoid-
XX producing plant comprising transforming a plant cell with a recombinant
XX construct comprising a promoter operably linked to a nucleic acid
XX sequence of at least 200 nucleotides having at least 75% sequence
XX identity to AD007965 (a soybean chalcone reductase cDNA). Also included
XX are an isoflavonoid-producing plant made by the method above, seeds or
XX plant parts of the plant, an isoflavonoid-containing protein product
XX having a reduced ratio of liguiritigenin-derived isoflavones relative to
XX the total isoflavone levels obtained from the seeds or plant parts, a
XX food (or a nutritional supplement, a food bar, or a beverage) which has
XX incorporated the isoflavonoid-containing product, and a method of
XX producing an isoflavonoid-containing product having a reduced ratio of
XX liguiritigenin-derived isoflavones relative to the total isoflavone
XX levels. The recombinant construct comprises a stem-loop structure. The
XX nucleic acid sequence forms a loop in the stem-loop structure and the
XX stem comprises a sequence of AD007968). The promoter is a seed-specific
XX promoter. The method is useful for decreasing the ratio of liguiritigenin-
XX derived isoflavones relative to the total isoflavones in an isoflavone-
XX producing plant. The methods and recombinant construct are useful in
XX producing an isoflavonoid-containing product which is incorporated in
XX cereal food product, snack food product, baked good product, fried food
XX product, health food product, infant formula, beverage, nutritional
XX supplement, dairy product, pet food product, or animal feed. The present
XX sequence is the seed specific gene silencing vector pKS151, into which
XX the soybean cDNA is cloned (into the NotI site flanked by the stem
XX regions of AD007968).

XX
SQ Sequence 7701 BP; 2236 A; 1702 C; 1709 G; 2053 T; 0 U; 1 Other;
SQ

Query Match 100.0%; Score 154; DB 12; Length 7701;
Best Local Similarity 100.0%; Pred. No. 3.1e-28;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 5604 CGGCGGAGCTGTCATCTCGCTCATCTGAGTCGGCGCGGAGCTGTCATCTGCT 5545
QY 61 CATGCTGAGTCGGCGCGCGCGGAGTCGAGATGACCAAGCTCCGGCGCGG 120
Db 5544 CATGCTGAGTCGGCGCGCGCGGAGTCGAGATGACCAAGCTCCGGCGCGG 5485
QY 121 ACTGACGATGAGCGAGATGACCAAGCTCCGGCGG 154
Db 5484 ACTGACGATGAGCGAGATGACCAAGCTCCGGCGG 5451

RESULT 13
ABK10072
ID ABK10072 standard; DNA; 4974 BP.
XX
AC ABK10072;
XX
DT 05-JUN-2002 (first entry)
XX
DE Plasmid pKS133 DNA.
XX
KW Plasmidic phosphoglucosylase; gene; ds; plasmid pKS133.
XX
OS Synthetic.
XX
XX EP1174510-A2.
XX
XX PD 23-JAN-2002.
XX

PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LJ,
XX WPI; 2002-156692/21.
DR
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
PS Example 9; SEQ ID NO 17; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC DNA used in the methods of the invention. Note: This sequence is not
CC represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX
SQ Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;
Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 4.5e-18;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCGGAGCTGATCTCGCTCATCTCGAGTCGGCGCGGAGCTGATCTCGCT 60
DB 4863 CGGCGGAGCTGATCTCGCTCATCTCGAGTCGGCGCGGAGCTGATCTCGCT 4922
QY 61 CATGTGTGAGTGGCGGCGCGGAGCTGAGCATGAGCGAGATCC 112
DB 4923 CATGTGTGAGTGGCGGCGCGGAGCTGAGCATGAGCGAGATCC 4974

RESULT 14
ABK10072/c
ID ABK10072 standard; DNA; 4974 BP.
XX
XX ABR10072;
XX
XX
DT 05-JUN-2002 (first entry)
XX
DE Plasmid pKS133 DNA.
XX
XX Plasmidic phosphoglucomutase; gene; ds; plasmid pKS133.
XX
OS Synthetic.
XX
XX EP1174510-A2.
XX
XX 23-JAN-2002.

PF 17-JUL-2001; 2001EP-00306143.
XX
PR 17-JUL-2000; 2000US-0218712P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Butler KH, Carlson TJ, Ilag LJ,
XX WPI; 2002-156692/21.
DR
XX
XX Novel isolated polypeptides having phosphoglucomutase activity and
PT polynucleotides encoding the polypeptides, useful for producing
PT transgenic plants with altered plastidic phosphoglucomutase protein
PT levels.
XX
PS Example 9; SEQ ID NO 17; 27pp; English.
XX
CC The invention relates to plastidic phosphoglucomutase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plastidic
CC phosphoglucomutase activity. An isolated polynucleotide that affects the
CC level of expression of a plastidic phosphoglucomutase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plastidic phosphoglucomutase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plastidic phosphoglucomutase. This sequence represents plasmid
CC DNA used in the methods of the invention. Note: This sequence is not
CC represented in the printed specification but is based on sequence
CC information supplied by the European Patent Office
XX
SQ Sequence 4974 BP; 1444 A; 1070 C; 1003 G; 1456 T; 0 U; 1 Other;
Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 4.5e-18;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 43 GAGCTGTGATCTCGCTCATCTCGAGTCGGCGCGGAGCTGAGCATGAGCGAGAT 102
DB 4974 GAGCTGTGATCTCGCTCATCTCGAGTCGGCGCGGAGCTGAGCATGAGCGAGAT 4915
QY 103 GACCACTCCGCGCGGAGCTGAGCATGAGCGAGATGACAGTCCGCGG 154
DB 4914 GACCACTCCGCGCGGAGCTGAGCATGAGCGAGATGACAGTCCGCGG 4863

RESULT 15
AAD32909
ID AAD32909 standard; DNA; 6611 BP.
XX
XX AAD32909;
XX
XX
DT 01-JUL-2002 (first entry)
XX
DE pBS68 plasmid used for diverged delta-9 desaturase suppression.
XX
XX Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
XX oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
XX
OS Unidentified.
XX
XX
XX Key Location/Qualifiers
FH 523..725
FT terminator
FT /*tag= b

```
FT      /label= Klt3_terminator
FT      complement(880..1920)
FT      /*tag= b
FT      /note= "Hygromycin selection region"
FT      promoter
FT      3260..5348
FT      /*tag= c
FT      /label= Klt3_promoter
XX
XX      WO200216565-A2.
XX
XX      28-FEB-2002.
XX
XX      22-AUG-2001; 2001WO-US026246.
XX
XX      22-AUG-2000; 2000US-0226996P.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS,
XX
XX      WPI; 2002-269353/31.
XX
XX      New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX      useful in creating transgenic plants having altered levels of mono-, poly
XX      - and unsaturated fatty acids and in increasing the unsaturation levels
XX      in cellular lipids.
XX
XX      Example 9; Page 76-77; 77pp; English.
XX
XX      The present invention relates to diverged delta-9 fatty acid desaturase
XX      proteins and polynucleotides encoding such proteins. The nucleic acid
XX      sequences may be used to increase the level of unsaturation in cellular
XX      lipids, including oil, in tissues when the enzyme is absent or rate-
XX      limiting, to isolate cDNAs and genes encoding homologous proteins from
XX      the same or other plant species and to create transgenic plants in which
XX      the polypeptides are present at higher or lower levels than normal or in
XX      cell types or developmental stages in which they are not normally found,
XX      thus altering the level of mono-, poly- and unsaturated fatty acids in
XX      those cells. They are useful as probes for genetic and physical gene
XX      mapping and as markers, e.g. restriction fragment length polymorphism
XX      (RFLP) markers. The peptides can be used to immunise animals to produce
XX      antibodies specific for the peptides and proteins. The present sequence
XX      is plasmid pBS68 which is used for the suppression of diverged delta-9
XX      desaturase in high stearate phenotypes. This sequence is used in the
XX      exemplification of the invention. Note: The sequence data for this
XX      sequence (AAD32909) corresponding to position 1501 to 6611 is not
XX      represented in the printed specification but is based on the sequence
XX      information supplied by the European patent office
XX
XX      Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 0 U; 1 Other;
SQ
Query Match      53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 5.4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGAGCTGTCATCTCGCT 60
Db      5348 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGAGCTGTCATCTCGCT 5407
OY      61 CATCTCGAGTCGGCGCGGCGGACT 86
Db      5408 CATCTCGAGTCGGCGCGGCGGCTGAGT 5433
XX
XX      RESULT 16
XX      AAD32909/c
XX      ID      AAD32909 standard; DNA; 6611 BP.
XX
XX      AC      AAD32909;
XX
XX      DT      01-JUL-2002 (first entry)
XX
XX      DE      pBS68 plasmid used for diverged delta-9 desaturase suppression.
```

```
XX      XX
XX      Rice; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;
XX      oil; transgenic plant; gene mapping; immunisation; plasmid pBS68; ds.
XX      Unidentified.
XX
XX      Key      Location/Qualifiers
XX      terminator      523..725
XX      /tag= b
XX      /label= Klt3_terminator
XX      complement(880..1920)
XX      misc_feature
XX      /*tag= b
XX      /note= "Hygromycin selection region"
XX      promoter
XX      3260..5348
XX      /*tag= c
XX      /label= Klt3_promoter
XX
XX      WO200216565-A2.
XX
XX      28-FEB-2002.
XX
XX      22-AUG-2001; 2001WO-US026246.
XX
XX      22-AUG-2000; 2000US-0226996P.
XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX      Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
XX      WPI; 2002-269353/31.
XX
XX      New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX      useful in creating transgenic plants having altered levels of mono-, poly
XX      - and unsaturated fatty acids and in increasing the unsaturation levels
XX      in cellular lipids.
XX
XX      Example 9; Page 76-77; 77pp; English.
XX
XX      The present invention relates to diverged delta-9 fatty acid desaturase
XX      proteins and polynucleotides encoding such proteins. The nucleic acid
XX      sequences may be used to increase the level of unsaturation in cellular
XX      lipids, including oil, in tissues when the enzyme is absent or rate-
XX      limiting, to isolate cDNAs and genes encoding homologous proteins from
XX      the same or other plant species and to create transgenic plants in which
XX      the polypeptides are present at higher or lower levels than normal or in
XX      cell types or developmental stages in which they are not normally found,
XX      thus altering the level of mono-, poly- and unsaturated fatty acids in
XX      those cells. They are useful as probes for genetic and physical gene
XX      mapping and as markers, e.g. restriction fragment length polymorphism
XX      (RFLP) markers. The peptides can be used to immunise animals to produce
XX      antibodies specific for the peptides and proteins. The present sequence
XX      is plasmid pBS68 which is used for the suppression of diverged delta-9
XX      desaturase in high stearate phenotypes. This sequence is used in the
XX      exemplification of the invention. Note: The sequence data for this
XX      sequence (AAD32909) corresponding to position 1501 to 6611 is not
XX      represented in the printed specification but is based on the sequence
XX      information supplied by the European patent office
XX
XX      Sequence 6611 BP; 1831 A; 1472 C; 1453 G; 1854 T; 0 U; 1 Other;
SQ
Query Match      53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 5.4e-11;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY      69 AGTCGGCGCGCGGATCGACGATGAGCGAGATGACCACTCGGCGCGGACTCGACG 128
Db      5433 ACTCAGCGCGCGGCGGATCGACGATGAGCGAGATGACCACTCGGCGCGGACTCGACG 5374
OY      129 ATGAGCGAGATGACCACTCGGCGG 154
Db      5373 ATGAGCGAGATGACCACTCGGCGG 5348
```

RESULT 17
ABK10711 standard; DNA; 81 BP.
XX ID ABK10711 standard; DNA; 81 BP.
XX AC ABK10711;
XX DT 05-JUN-2002 (first entry)
XX DE Artificial DNA sequence #3.
XX KM Plasmidic phosphoglucumutase; transgenic; plant; gene; ds.
XX OS Synthetic.
XX FH Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT CDS 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX EP1174510-A2.
XX 23-JAN-2002.
XX 17-JUL-2001; 2001EP-00306143.
XX 17-JUL-2000; 2000US-0218712P.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Allen SM, Butler KH, Carlson TV, Ilag LL;
XX WPI; 2002-156692/21.
XX P-PSDB; AAU77109.
XX Novel isolated polypeptides having phosphoglucumutase activity and
XX transgenic plants encoding the polypeptides, useful for producing
XX transgenic plants with altered plasmidic phosphoglucumutase protein
XX levels.
XX Example 9; Page 19; 27pp; English.
XX The invention relates to plasmidic phosphoglucumutase polypeptides and
XX their related nucleic acids. The sequences are useful for producing a
XX transgenic plant, by transforming a plant cell with a polynucleotide of
XX the invention and regenerating a plant from the transformed plant cell.
XX Polynucleotide fragments are useful for suppressing the level of
XX expression of a gene encoding a polypeptide having plasmidic
XX phosphoglucumutase activity. An isolated polynucleotide that affects the
XX level of expression of a plasmidic phosphoglucumutase polypeptide in a
XX plant cell can be identified by introducing a DNA fragment comprising at
XX least 541 nucleotides, measuring the level of the polypeptide in the
XX plant cell containing the polynucleotide, and comparing the level of the
XX polypeptide in the plant cell containing the isolated polynucleotide with
XX the level of the polypeptide in a plant cell that does not contain the
XX isolated polynucleotide. A method for altering the level of expression of
XX a plasmidic phosphoglucumutase protein in a host cell comprises
XX transforming a host cell with a chimeric gene and growing the transformed
XX cell under conditions that are suitable for expression of the chimeric
XX gene, where the expression of the gene results in production of altered
XX levels of plasmidic phosphoglucumutase. This sequence represents an
XX artificial DNA used for plasmid construction, in the methods of the
XX invention
XX Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;
XX Query Match 52.6%; Score 81; DB 6; Length 81;

Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGAGCTGCTCATCTGCTCATCTGAGCGGCGGCGGAGCTGCTCATCTGCT 60
Db 1 CGGCGGAGCTGCTCATCTGCTCATCTGAGCGGCGGCGGAGCTGCTCATCTGCT 60
Qy 61 CATGCTGAGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 81
Db 61 CATGCTGAGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 81
RESULT 18
ABK10711/c
XX ID ABK10711 standard; DNA; 81 BP.
XX AC ABK10711;
XX DT 05-JUN-2002 (first entry)
XX DE Artificial DNA sequence #3.
XX KM Plasmidic phosphoglucumutase; transgenic; plant; gene; ds.
XX OS Synthetic.
XX FH Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
FT CDS 44..73
FT /*tag= b
FT /product= "ELVISLIVES peptide"
FT /partial
FT /note= "No start or stop codon shown"
XX EP1174510-A2.
XX 23-JAN-2002.
XX 17-JUL-2001; 2001EP-00306143.
XX 17-JUL-2000; 2000US-0218712P.
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX Allen SM, Butler KH, Carlson TV, Ilag LL;
XX WPI; 2002-156692/21.
XX P-PSDB; AAU77109.
XX Novel isolated polypeptides having phosphoglucumutase activity and
XX transgenic plants encoding the polypeptides, useful for producing
XX transgenic plants with altered plasmidic phosphoglucumutase protein
XX levels.
XX Example 9; Page 19; 27pp; English.
XX The invention relates to plasmidic phosphoglucumutase polypeptides and
XX their related nucleic acids. The sequences are useful for producing a
XX transgenic plant, by transforming a plant cell with a polynucleotide of
XX the invention and regenerating a plant from the transformed plant cell.
XX Polynucleotide fragments are useful for suppressing the level of
XX expression of a gene encoding a polypeptide having plasmidic
XX phosphoglucumutase activity. An isolated polynucleotide that affects the
XX level of expression of a plasmidic phosphoglucumutase polypeptide in a
XX plant cell can be identified by introducing a DNA fragment comprising at
XX least 541 nucleotides, measuring the level of the polypeptide in the
XX plant cell containing the polynucleotide, and comparing the level of the
XX polypeptide in the plant cell containing the isolated polynucleotide with
XX the level of the polypeptide in a plant cell that does not contain the

CC isolated polynucleotide. A method for altering the level of expression of
CC a plasmidic phosphoglucosyltransferase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plasmidic phosphoglucosyltransferase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention
XX
SQ Sequence 81 BP; 8 A; 28 C; 29 G; 16 T; 0 U; 0 Other;
Query Match 52.6%; Score 81; DB 6; Length 81;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 GCGGCGCCGACTCGAGATGAGCGAGATGACCACTCCGCGCGGACTCGAGATGAG 133
DB 81 GCGGCGCCGACTCGAGATGAGCGAGATGACCACTCCGCGCGGACTCGAGATGAG 22
QY 134 CGAGATGACCACTCCGCGCG 154
DB 21 CGAGATGACCACTCCGCGCG 1
RESULT 19
AAD29247
ID AAD29247 standard; DNA; 963 BP.
XX
AC AAD29247;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmid pBS149 2X ELVISLIVES complementary region DNA.
XX
KM Recombinant construct; gene expression; late-soybean-embryo promoter;
KM LBA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
XX
OS Unidentified.
XX
OS WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 10; Page 72; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from

CC it. The present sequence is 2X ELVISLIVES complementary region from
CC pBS149 that contains fragments from two soybean galactinol synthase genes
CC GAS1 and GAS2. The region is functionally attached to a late-soybean
CC embryo promoter (LBA) and a phaseolin 3' terminator region. This entire
CC region is then cloned into BamHI site of pBS136, which contains a 2X
CC ELVISLIVES complementary region controlled by a soybean K1 promoter and
CC terminator region used in the exemplification of the invention
XX
SQ Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 U; 0 Other;
Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 GCGGCGCCGACTCGAGATGAGCGAGATGACCACTCCGCGCGGACTCGAGATGAG 133
DB 883 GCGGCGCCGACTCGAGATGAGCGAGATGACCACTCCGCGCGGACTCGAGATGAG 942
QY 134 CGAGATGACCACTCCGCGCG 154
DB 943 CGAGATGACCACTCCGCGCG 963
RESULT 20
AAD29247/C
ID AAD29247 standard; DNA; 963 BP.
XX
AC AAD29247;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmid pBS149 2X ELVISLIVES complementary region DNA.
XX
KM Recombinant construct; gene expression; late-soybean-embryo promoter;
KM LBA; galactinol synthase; GAS1; GAS2; plasmid pBS149; ds.
XX
OS Unidentified.
XX
OS WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Example 10; Page 72; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 2X ELVISLIVES complementary region from

CC pBS149 that contains fragments from two soybean galactinol synthase genes
CC GAS1 and GAS2. The region is functionally attached to a late-soybean-
CC embryo promoter (LEA) and a phaseolin 3' terminator region. This entire
CC region is then cloned into BamHI site of pKS16, which contains a 2X
CC ELVISLIVES complementary region controlled by a soybean Kti promoter and
CC terminator region used in the exemplification of the invention
XX
SQ Sequence 963 BP; 240 A; 243 C; 248 G; 232 T; 0 U; 0 Other;
Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 1.4e-10;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTGCT 60
Db 963 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTGCT 904
Qy 61 CATGTCGAGTCGGCGCGCGC 81
Db 903 CATGTCGAGTCGGCGCGCGC 883
RESULT 21
AAD29230
ID AAD29230 standard; DNA; 80 BP.
XX
AC AAD29230;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KM Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
XX ds.
OS Unidentified.
XX
PH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT CDS complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
PN WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX P-PSDB; AAE18333.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Claim 45; Page 37; 77pp; English.
XX
CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The

CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 38 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTGCT 97
Db 1 CGGCGGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGAGCTGTCATCTGCT 60
Qy 98 GAGATGACCAAGCTCCGCCG 117
Db 61 GAGATGACCAAGCTCCGCCG 80
RESULT 22
AAD29230/c
ID AAD29230 standard; DNA; 80 BP.
XX
AC AAD29230;
XX
DT 07-MAY-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KM Recombinant construct; gene expression; plasmid pKS124; plasmid pKS106;
XX ds.
OS Unidentified.
XX
PH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT CDS complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
PN WO200200904-A2.
XX
PD 03-JAN-2002.
XX
PF 22-JUN-2001; 2001WO-US019962.
XX
PR 23-JUN-2000; 2000US-0213961P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL,
PI Nichols SE;
XX
DR WPI; 2002-139927/18.
XX P-PSDB; AAE18333.
XX
PT New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.
XX
PS Claim 45; Page 37; 77pp; English.
XX

CC The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC when expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is 1X ELVISLIVES complementary repeat region DNA
CC found in plasmids pKS106 and pKS124 used in the exemplification of the
CC invention
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGGCCGCACTCGACATGAGC 97
DB 80 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGGCCGCACTCGACATGAGC 21
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 20 GAGATGACCAAGCTCCGGCCG 1
RESULT 23
AAD32907
ID AAD32907 standard; DNA; 80 BP.
AC AAD32907;
XX
DT 01-JUL-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KM Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
KM transgenic plant; gene mapping; immunisation; plasmid pKS124;
KM plasmid pKS106; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX MO200216565-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026246.
XX
XX 22-AUG-2000; 2000US-0226996P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
XX WPI; 2002-269353/31.
XX
XX P-PSDB; AAE20554.
XX
XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
XX useful in creating transgenic plants having altered levels of mono-, poly
XX - and unsaturated fatty acids and in increasing the unsaturation levels
XX in cellular lipids.
PT
PT

XX
XX Example 9; Page 43; 77pp; English.
XX
PS The present invention relates to diverged delta-9 fatty acid desaturase
CC proteins and polynucleotides encoding such proteins. The nucleic acid
CC sequences may be used to increase the level of unsaturation in cellular
CC lipids, including oil, in tissues when the enzyme is absent or rate-
CC limiting, to isolate cDNAs and genes encoding homologous proteins from
CC the same or other plant species and to create transgenic plants in which
CC the polypeptides are present at higher or lower levels than normal or in
CC cell types or developmental stages in which they are not normally found,
CC thus altering the level of mono-, poly- and unsaturated fatty acids in
CC those cells. They are useful as probes for genetic and physical gene
CC mapping and as markers, e.g. restriction fragment length polymorphism
CC (RFLP) markers. The peptides can be used to immunise animals to produce
CC antibodies specific for the peptides and proteins. The present sequence
CC is 1X ELVISLIVES complementary repeat region DNA found in plasmids pKS106
CC and pKS124. This sequence is used in the exemplification of the invention
CC for the suppression of Fad2 in soybean
XX
SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 2.2e-10;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGGCCGCACTCGACATGAGC 97
DB 1 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGGCCGCACTCGACATGAGC 60
QY 98 GAGATGACCAAGCTCCGGCCG 117
DB 61 GAGATGACCAAGCTCCGGCCG 80
RESULT 24
AAD32907/C
ID AAD32907 standard; DNA; 80 BP.
AC AAD32907;
XX
DT 01-JUL-2002 (first entry)
XX
DE Plasmids pKS106, pKS124 1X ELVISLIVES complementary repeat DNA.
XX
KM Diverged delta-9 fatty acid desaturase; enzyme; cellular lipid; oil;
KM transgenic plant; gene mapping; immunisation; plasmid pKS124;
KM plasmid pKS106; gene; ds.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT CDS 7..36
FT /*tag= a
FT /product= "ELVISLIVES protein"
FT complement(45..74)
FT /*tag= b
FT /product= "ELVISLIVES protein"
XX
XX MO200216565-A2.
XX
XX 28-FEB-2002.
XX
XX 22-AUG-2001; 2001WO-US026246.
XX
XX 22-AUG-2000; 2000US-0226996P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;
XX
XX WPI; 2002-269353/31.
XX
XX P-PSDB; AAE20554.
XX
XX

XX New delta-9 fatty acid desaturase polypeptides and polynucleotides,
 PT useful in creating transgenic plants having altered levels of mono-, poly
 PT - and unsaturated fatty acids and in increasing the unsaturation levels
 PT in cellular lipids.
 XX
 PS Example 9; Page 43; 77pp; English.
 CC The present invention relates to diverged delta-9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rate-
 CC limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is IX BLVSLIVES complementary repeat region DNA found in plasmids pXS106
 CC and pXS124. This sequence is used in the exemplification of the invention
 CC for the suppression of Pad2 in soybean
 CC
 CC
 SQ Sequence 80 BP; 12 A; 28 C; 28 G; 12 T; 0 U; 0 Other;
 Query Match 51.9%; Score 80; DB 6; Length 80;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTGGCGCGCGGACTCGACGATGAGC 97
 Db 80 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTGGCGCGCGGACTCGACGATGAGC 21
 QY 98 GAGATGACCAAGCTCCGGCCG 117
 Db 20 GAGATGACCAAGCTCCGGCCG 1
 RESULT 25
 ABK10712
 ID ABK10712 standard; DNA; 92 BP.
 AC ABK10712;
 XX 05-JUN-2002 (first entry)
 DT
 XX Artificial DNA sequence #4.
 DE
 XX Plasmidic phosphoglucumutase; transgenic; plant; gene; ss.
 KM
 XX Synthetic.
 OS
 XX EP1174510-A2.
 PN
 XX 23-JAN-2002.
 PD
 XX 17-JUL-2001; 2001EP-00306143.
 PF
 XX 17-JUL-2000; 2000US-0218712P.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 PI Allen SM, Butler KH, Carlson TJ, Ilag LJ;
 XX
 XX MPI; 2002-156692/21.
 DR
 XX Novel isolated polypeptides having phosphoglucumutase activity and
 PT polynucleotides encoding the polypeptides, useful for producing
 PT transgenic plants with altered plasmidic phosphoglucumutase protein
 PT levels.
 XX

PS Example 9; Page 19; 27pp; English.
 CC The invention relates to plasmidic phosphoglucumutase polypeptides and
 CC their related nucleic acids. The sequences are useful for producing a
 CC transgenic plant, by transforming a plant cell with a polynucleotide of
 CC the invention and regenerating a plant from the transformed plant cell.
 CC Polynucleotide fragments are useful for suppressing the level of
 CC expression of a gene encoding a polypeptide having plasmidic
 CC phosphoglucumutase activity. An isolated polynucleotide that affects the
 CC level of expression of a plasmidic phosphoglucumutase polypeptide in a
 CC plant cell can be identified by introducing a DNA fragment comprising at
 CC least 541 nucleotides, measuring the level of the polypeptide in the
 CC plant cell containing the polynucleotide, and comparing the level of the
 CC polypeptide in the plant cell containing the isolated polynucleotide with
 CC the level of the polypeptide in a plant cell that does not contain the
 CC isolated polynucleotide. A method for altering the level of expression of
 CC a plasmidic phosphoglucumutase protein in a host cell comprises
 CC transforming a host cell with a chimeric gene and growing the transformed
 CC cell under conditions that are suitable for expression of the chimeric
 CC gene, where the expression of the gene results in production of altered
 CC levels of plasmidic phosphoglucumutase. This sequence represents an
 CC artificial DNA used for plasmid construction, in the methods of the
 CC invention
 CC
 CC
 SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;
 Query Match 51.9%; Score 80; DB 6; Length 92;
 Best Local Similarity 100.0%; Pred. No. 2.2e-10;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 38 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTGGCGCGCGGACTCGACGATGAGC 97
 Db 7 CGGCGGAGCTGTCATCTCGCTCATCGTCGAGTGGCGCGCGGACTCGACGATGAGC 66
 QY 98 GAGATGACCAAGCTCCGGCCG 117
 Db 67 GAGATGACCAAGCTCCGGCCG 86
 RESULT 26
 ABK10712/c
 ID ABK10712 standard; DNA; 92 BP.
 AC ABK10712;
 XX 05-JUN-2002 (first entry)
 DT
 XX Artificial DNA sequence #4.
 DE
 XX Plasmidic phosphoglucumutase; transgenic; plant; gene; ss.
 KM
 XX Synthetic.
 OS
 XX EP1174510-A2.
 PN
 XX 23-JAN-2002.
 PD
 XX 17-JUL-2001; 2001EP-00306143.
 PF
 XX 17-JUL-2000; 2000US-0218712P.
 PR
 XX (DUPO) DU PONT DE NEMOURS & CO E I.
 PA
 PI Allen SM, Butler KH, Carlson TJ, Ilag LJ;
 XX
 XX MPI; 2002-156692/21.
 DR
 XX Novel isolated polypeptides having phosphoglucumutase activity and
 PT polynucleotides encoding the polypeptides, useful for producing
 PT transgenic plants with altered plasmidic phosphoglucumutase protein
 PT levels.
 XX Example 9; Page 19; 27pp; English.
 PS

XX The invention relates to plasmidic phosphoglucosyltransferase polypeptides and
CC their related nucleic acids. The sequences are useful for producing a
CC transgenic plant, by transforming a plant cell with a polynucleotide of
CC the invention and regenerating a plant from the transformed plant cell.
CC Polynucleotide fragments are useful for suppressing the level of
CC expression of a gene encoding a polypeptide having plasmidic
CC phosphoglucosyltransferase activity. An isolated polynucleotide that affects the
CC level of expression of a plasmidic phosphoglucosyltransferase polypeptide in a
CC plant cell can be identified by introducing a DNA fragment comprising at
CC least 541 nucleotides, measuring the level of the polypeptide in the
CC plant cell containing the polynucleotide, and comparing the level of the
CC polypeptide in the plant cell containing the isolated polynucleotide with
CC the level of the polypeptide in a plant cell that does not contain the
CC isolated polynucleotide. A method for altering the level of expression of
CC a plasmidic phosphoglucosyltransferase protein in a host cell comprises
CC transforming a host cell with a chimeric gene and growing the transformed
CC cell under conditions that are suitable for expression of the chimeric
CC gene, where the expression of the gene results in production of altered
CC levels of plasmidic phosphoglucosyltransferase. This sequence represents an
CC artificial DNA used for plasmid construction, in the methods of the
CC invention

XX SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;

Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGATCGAGTGGCGCGCCGCACTGCAGCATGAGC 97

Db 86 CGGCCGAGCTGTCATCTCGCTCATCTCGATCGAGTGGCGCGCCGCACTGCAGCATGAGC 27

OY 98 GAGATGACCACTCGCGCGC 117

Db 26 GAGATGACCACTCGCGCGC 7

RESULT 27

AAD29232
ID AAD29232 standard; DNA; 92 BP.

XX AAD29232;

DT 07-MAY-2002 (first entry)

DE ELVISLIVES complementary region DNA amplifying PCR primer #1.

XX Recombinant construct; gene expression; PCR primer; ss.

OS Unidentified.

XX WO200200904-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US019962.

XX 23-JUN-2000; 2000US-0213961P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;

XX Nichols SE;

XX WPI; 2002-139927/18.

XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

PS Example 7; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC target mRNA expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target
CC mRNA or any similar endogenous mRNA. The RNAs expressed from the
CC recombinant constructs are also used in reducing expression of a target
CC mRNA or any similar endogenous mRNA. The sequences and their reverse
CC complements can be used to reduce the expression of any endogenous
CC genomic sequence that shares substantial similarity to nucleic acid
CC fragment which is in proximity to the DNA or RNA sequence derived from
CC it. The present sequence is a PCR primer used for amplifying ELVISLIVES
CC complementary region DNA used in the exemplification of the invention

XX SQ Sequence 92 BP; 16 A; 30 C; 30 G; 16 T; 0 U; 0 Other;

Query Match 51.9%; Score 80; DB 6; Length 92;

Best Local Similarity 100.0%; Pred. No. 2.2e-10; Mismatches 0; Indels 0; Gaps 0;

Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGATCGAGTGGCGCGCCGCACTGCAGCATGAGC 97

Db 7 CGGCCGAGCTGTCATCTCGCTCATCTCGATCGAGTGGCGCGCCGCACTGCAGCATGAGC 66

OY 98 GAGATGACCACTCGCGCGC 117

Db 67 GAGATGACCACTCGCGCGC 86

RESULT 28
AAD29232/c
ID AAD29232 standard; DNA; 92 BP.

XX AAD29232;

DT 07-MAY-2002 (first entry)

DE ELVISLIVES complementary region DNA amplifying PCR primer #1.

XX Recombinant construct; gene expression; PCR primer; ss.

OS Unidentified.

XX WO200200904-A2.

XX 03-JAN-2002.

XX 22-JUN-2001; 2001WO-US019962.

XX 23-JUN-2000; 2000US-0213961P.

XX (DUPO) DU PONT DE NEMOURS & CO E I.

XX (PION-) PIONEER HI-BRED INT INC.

XX Glassman KF, Gordon-Kamm WJ, Kinney AJ, Lowe K, Stecca KL;

XX Nichols SE;

XX WPI; 2002-139927/18.

XX New recombinant construct having a promoter operably linked to a DNA
PT sequence which when expressed produces an RNA having homology to a target
PT mRNA and its reverse complement unrelated to endogenous DNA, for reducing
PT gene expression.

XX Example 7; Page 37; 77pp; English.

XX The present invention relates to a new recombinant construct. The
CC construct comprises a promoter operably linked to a DNA sequence which
CC target mRNA expressed by a host produces an RNA having homology to at least one
CC target mRNA expressed by the host and complementary RNA regions. The
CC recombinant construct is useful for reducing the expression of a target

Query Match 29.7%; Score 45.8; DB 6; Length 1717;
 Best Local Similarity 95.9%; Pred. No. 0.048; 2; Indels 0; Gaps 0;
 Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

69 AGTCGGCGCGCCGCTCGACGATGAGCGAGATGACAGCTCCGGCG 117
 49 ACTGAGCGCGCGCGCTCGACGATGAGCGAGATGACAGCTCCGGCG 1

Db

RESULT 31
 ABK10710
 ID ABK10710 standard; DNA; 44 BP.
 XX
 AC ABK10710;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Artificial DNA sequence #2.
 XX
 KW Plastidic phosphoglucumutase; transgenic; plant; gene; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag= a
 FT /product= "ELVISLIVES peptide"
 FT /partial
 FT /note= "No start or stop codon shown"

EP1174510-A2.
 XX
 PD 23-JAN-2002.
 XX
 PF 17-JUL-2001; 2001EP-00306143.
 XX
 PR 17-JUL-2000; 2000US-0218712P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Allen SM, Butler KH, Carlson TV, Ilag LL;
 XX
 DR WPI: 2002-156692/21.
 DR P-PSDB; AAU77109.
 XX
 PT Novel isolated polypeptides having phosphoglucumutase activity and
 PT polynucleotides encoding the polypeptides, useful for producing
 PT transgenic plants with altered plastidic phosphoglucumutase protein
 PT levels.
 XX
 PS Example 9; Page 19; 27pp; English.
 XX
 CC The invention relates to plastidic phosphoglucumutase polypeptides and
 CC their related nucleic acids. The sequences are useful for producing a
 CC transgenic plant, by transforming a plant cell with a polynucleotide of
 CC the invention and regenerating a plant from the transformed plant cell.
 CC Polynucleotide fragments are useful for suppressing the level of
 CC expression of a gene encoding a polypeptide having plastidic
 CC phosphoglucumutase activity. An isolated polynucleotide that affects the
 CC level of expression of a plastidic phosphoglucumutase polypeptide in a
 CC plant cell can be identified by introducing a DNA fragment comprising at
 CC least 541 nucleotides, measuring the level of the polypeptide in the
 CC plant cell containing the polynucleotide, and comparing the level of the
 CC polypeptide in the plant cell containing the isolated polynucleotide with
 CC the level of the polypeptide in a plant cell that does not contain the
 CC isolated polynucleotide. A method for altering the level of expression of
 CC a plastidic phosphoglucumutase protein in a host cell comprises
 CC transforming a host cell with a chimeric gene and growing the transformed
 CC cell under conditions that are suitable for expression of the chimeric
 CC gene, where the expression of the gene results in production of altered
 CC levels of plastidic phosphoglucumutase. This sequence represents an
 CC artificial DNA used for plasmid construction, in the methods of the

CC invention
 XX

SO Sequence 44 BP; 4 A; 16 C; 16 G; 8 T; 0 U; 0 Other;
 Query Match 28.6%; Score 44; DB 6; Length 44;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

38 CGGCGGAGCGTGGTCATCGTCATCGTCAGTGGGCGCG 81
 1 CGGCGGAGCGTGGTCATCGTCATCGTCAGTGGGCGCG 44

Db

RESULT 32
 ABK10710/c
 ID ABK10710 standard; DNA; 44 BP.
 XX
 AC ABK10710;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Artificial DNA sequence #2.
 XX
 KW Plastidic phosphoglucumutase; transgenic; plant; gene; ds.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT CDS 7..36
 FT /*tag= a
 FT /product= "ELVISLIVES peptide"
 FT /partial
 FT /note= "No start or stop codon shown"

EP1174510-A2.
 XX
 PD 23-JAN-2002.
 XX
 PF 17-JUL-2001; 2001EP-00306143.
 XX
 PR 17-JUL-2000; 2000US-0218712P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Allen SM, Butler KH, Carlson TV, Ilag LL;
 XX
 DR WPI: 2002-156692/21.
 DR P-PSDB; AAU77109.
 XX
 PT Novel isolated polypeptides having phosphoglucumutase activity and
 PT polynucleotides encoding the polypeptides, useful for producing
 PT transgenic plants with altered plastidic phosphoglucumutase protein
 PT levels.
 XX
 PS Example 9; Page 19; 27pp; English.
 XX
 CC The invention relates to plastidic phosphoglucumutase polypeptides and
 CC their related nucleic acids. The sequences are useful for producing a
 CC transgenic plant, by transforming a plant cell with a polynucleotide of
 CC the invention and regenerating a plant from the transformed plant cell.
 CC Polynucleotide fragments are useful for suppressing the level of
 CC expression of a gene encoding a polypeptide having plastidic
 CC phosphoglucumutase activity. An isolated polynucleotide that affects the
 CC level of expression of a plastidic phosphoglucumutase polypeptide in a
 CC plant cell can be identified by introducing a DNA fragment comprising at
 CC least 541 nucleotides, measuring the level of the polypeptide in the
 CC plant cell containing the polynucleotide, and comparing the level of the
 CC polypeptide in the plant cell containing the isolated polynucleotide with
 CC the level of the polypeptide in a plant cell that does not contain the
 CC isolated polynucleotide. A method for altering the level of expression of
 CC a plastidic phosphoglucumutase protein in a host cell comprises
 CC transforming a host cell with a chimeric gene and growing the transformed
 CC cell under conditions that are suitable for expression of the chimeric

Db 1.1.8 AGCGCTGGACCAAGTGC GG GTGACGATCATCAGCAGC 1080

RESULT 35
ADJ4005
ID ADJ4005 standard; cDNA; 2730 BP.

AC	ADJ40055;	
XX		
DT	06-MAY-2004	(first entry)

KM plant, gene, ss; transcription; plant genome augmentation; cereal;
KM soybean; allelic; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.

PA	(BUDM/	BUDWORTH P.
PA	(MOUG/	MOUGHAMER T.
PA	(BRIG/	BRIGHTS S P.
PA	(COOP/	COOPER B.
PA	(GLAZ/	GLAZEBROOK J.
PA	(GOLF/	GOLF S A.
PA	(KATA/	KATAGIRI F.
PA	(KREP/	KREPS J.
PA	(PROV/	PROVART N.
PA	(RICK/	RICKE D.
PA	(ZHUT/	ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Golf SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;

DR WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 25; SEQ ID NO 1055; 230pp; English.

The invention relates to plant nucleotide sequences that direct seed-, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polynucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant nucleic acid of the invention. Note: The sequence data for this

CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 2730 BP; 470 A; 1009 C; 847 G; 400 T; 0 U; 4 Other;

Query Match	22.9%	Score 35.2	DB 12	Length 2730
Best Local Similarity	56.6%	Pred. No. 18		
Matches 64; Conservative	0	Mismatches 49	Indels 0	Gaps 0

```

Oy      1  CGCCGAGCGTCATCTCGTCATCGTAGCGGCGGAGCTGGTCATCTCGCT 60
        |||||  |||||  |||||  |||||  |||||  |||||
Db      31  CGGCAAGCGCTCCAGTCGCTGACACGCGTTGCTGCTGGCGGCTGGCGCT 90

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```

Oy      61 CATCGTCGAGTCGGCGCGCGCGGATCTCGACGATGACGAGTACCGAGTCCG 113
      :  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      91 CGTCGTGGCGGCGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 143

```

RESULT 36
ADJ40055/c
ID ADJ40055 standard; cDNA; 2730 BP.

AC ADJ40055;

DT 06-MAY-2004 (first entry)

DE Plant cDNA #1055.

KM plant; gene; ss; transcripition; plant genome augmentation; cereal;
 KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet
 KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
 KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
 KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
 KM antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004

PR 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.
PR 26-SEP-2001; 2001US-0325448P.
PR 04-APR-2002; 2002US-0370620P.

PA (BUDM/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOB/) COOPER B.
PA (GLAZ/) GLAZEBROOK J
PA (GOFB/) GOF S A.
PA (KATN/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVART N.
PA (RICK/) RICE D.
PA (ZHUT/) ZHU T.

xx Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J
 PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T,
 XX WPI: 2004-190374/18.

PT New rice promoter, 1

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 25; SEQ ID NO 1055; 230pp; English

CC The invention relates to plant nucleotide sequences that direct seed-, CC
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

Sequence 2730 BP; 470 A; 1009 C; 847 G; 400 T; 0 U; 4 Other;

Query Match 22.9%; Score 35.2; DB 12; Length 2730;
Best Local Similarity 56.6%; Pred. No. 18; Mismatches 49; Indels 0; Gaps 0;
Matches 64; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 42 CGGAGCTGTCATCTCGCTCATCTGTCGATCGCGCGCCGCGACTCGACGATGAGCGAGA 101
Db 143 CCGGGCTGTACAGCTTCGCGCGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 84

Qy 102 TGACCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 154
Db 83 GCGGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 31

RESULT 37
ACH91679 standard; DNA; 850 BP.

XX ACH91679;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #24874.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX
XX (RANK/) RANK D R.
XX
XX (HANZ/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI: 2004-119264/12.
XX
XX
XX New human genome-derived single exon nucleic acid probes useful for human
XX gene expression analysis, for identifying or characterizing alternative
XX splicing events, for assessing genomic alterations or as tools for
XX surveying tissues.
XX
XX
XX Claim 1; SEQ ID NO 24874; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
XX expression, comprising any of the 27,400 fully defined nucleotide
XX sequences in the specification, or their complements or fragments, and

CC encoding at least 8 amino acids of any of the 6888 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridises under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subsequence, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterising
CC alternative splicing events, in detecting and characterising gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in printing the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030194704
XX

Sequence 850 BP; 111 A; 291 C; 362 G; 86 T; 0 U; 0 Other;

Query Match 22.7%; Score 35; DB 12; Length 850;
Best Local Similarity 56.5%; Pred. No. 19; Mismatches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 39 GCGCGAGCTGTCATCTCGCTCATCTGTCGATCGCGCGCGCGCGCGCGCGCGCGCGCG 98
Db 375 GCGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 434

Qy 99 AGATGACCACTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 153
Db 435 TCGTGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 489

RESULT 38
ACH91679/c
ID ACH91679 standard; DNA; 850 BP.

XX ACH91679;
XX
XX 29-JUL-2004 (first entry)
XX
XX Human genome derived single exon probe #24874.
XX
XX Human; probe; ss; gene expression; single exon probe; microarray;
XX
XX alternative splicing event; genomic alteration.
XX
XX Homo sapiens.
XX
XX US2003194704-A1.
XX
XX 16-OCT-2003.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX 03-APR-2002; 2002US-00029386.
XX
XX (PENN/) PENN S G.
XX
XX (RANK/) RANK D R.

PA (HANEL/) HANZEL D K.
XX
XX Penn SG, Rank DR, Hanzel DK;
XX
XX WPI; 2004-119264/12.
XX
XX New human genome-derived single exon nucleic acid probes useful for human
PT gene expression analysis, for identifying or characterizing alternative
PT splicing events, for assessing genomic alterations or as tools for
PT surveying tissues.
XX
XX Claim 1; SEQ ID NO 24674; 80pp; English.
XX
XX The invention relates to a nucleic acid probe for measuring human gene
CC expression, comprising any of the 27,400 fully defined nucleotide
CC sequences in the specification, or their complements or fragments, and
CC encoding at least 8 amino acids of any of the 688 amino acid sequences
CC fully defined in the specification. The probe is a single exon probe that
CC hybridizes under high stringency conditions to a nucleic acid molecule
CC expressed in human cells or tissues. Also included are a spatially-
CC addressable set of single exon nucleic acid probes for measuring human
CC gene expression (comprising a plurality of single exon nucleic acid
CC probes cited above, where each of the plurality of probes is separately
CC and addressably isolatable or amplifiable from the plurality), a single
CC exon microarray for measuring human gene expression, a method of
CC measuring human gene expression, a vector comprising the single exon
CC probe cited above, an ORF-encoded peptide comprising at least 8
CC contiguous amino acids of any of the above-mentioned amino acid
CC sequences (optionally with conservative amino acid substitutions), an
CC isolated antibody that binds specifically to a peptide cited above,
CC methods of selling and/or licensing single exon probes or microarrays to
CC a customer desiring to measure gene expression, a method of providing
CC human gene expression data by subcription, and a computer-readable
CC storage medium which contains a database having a plurality of records
CC (each record including data on the expression of a single exon probe
CC cited above. The probe, methods and apparatus are useful in gene
CC expression analysis. The probes may be used as tools for surveying
CC tissues to detect the presence of expressed messages that contain their
CC specific exon, or in constructing genome-derived single exon microarrays.
CC In addition, the probes are used in identifying and characterizing
CC alternative splicing events, in detecting and characterizing gross
CC alterations in the genomic locus that includes their exon, in assessing
CC smaller genomic alterations, in priming the synthesis of nucleic acids,
CC or in expressing the ORF-encoded peptide. The present sequence is a human
CC single exon probe of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docID=20030194704
XX
XX Sequence 850 BP; 111 A; 291 C; 362 G; 86 T; 0 U; 0 Other;
SQ
Query Match 22.7%; Score 35; DB 12; Length 850;
Best Local Similarity 56.5%; Pred. No. 19;
Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 2 GGGCGAGCTGTATCTCGCTCATCTGCGAGTGGCGGCGGAGCTGTATCTGCTC 61
Db 489 GGGCGAGCTGTATCTCGCTCATCTGCGAGTGGCGGCGGAGCTGTATCTGCTC 61
QY 62 ATCGTCAGTGGCGGCGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 116
Db 429 GCGTCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 375
RESULT 39
ADP24630
ID ADP24630 standard; cDNA; 1797 BP.
XX
XX AC ADP24630;
XX
XX 18-NOV-2004 (first entry)
XX
XX PRO polypeptide encoding cDNA SEQ ID NO:1808.

XX
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
XX immunosuppressive; osteoporotic; antidiabetic; dermatological;
XX antipsoriatic; antiallergic; antiaslathmic; hepatotropic; respiratory;
XX gene therapy; immune system.
XX
XX Unidentified.
XX
XX WO2004041170-A2.
XX
XX 21-MAY-2004.
XX
XX 30-OCT-2003; 2003WO-US034312.
XX
XX 01-NOV-2002; 2002US-0423394P.
XX
XX (GENTH) GENENTECH INC.
XX
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX Wu TD;
XX WPI; 2004-419628/39.
XX P-PSDB; ADP24631.
XX
XX New PRO polypeptides and polynucleotides, useful for treating e.g.
PT renal disease, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT nervous system.
XX
XX Claim 1; SEQ ID NO 1808; 2940pp; English.
XX
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antirheumatic, antiarthritic, antirheumatic, immunosuppressive,
XX osteoporotic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX antiaslathmic, hepatotropic, and respiratory activity. A polynucleotide
XX of the invention may have a use in gene therapy. The PRO polypeptide, its
XX agonist, antagonist, or antibody that specifically binds to the
XX polypeptide is useful for treating an immune related disorder such as
XX systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX disease, a demyelinating disease of the central or peripheral nervous
XX system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX disease, infectious or autoimmune chronic active hepatitis, primary
XX biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX disease, asthma, allergic rhinitis, atopic dermatitis, food
XX hypersensitivity, urticaria, an immunologic disease of the lung,
XX eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX pneumonitis, a transplantation associated disease, graft rejection or
XX graft-versus-host disease. The present sequence encodes a PRO protein of
XX the invention.
SQ
Sequence 1797 BP; 263 A; 645 C; 552 G; 337 T; 0 U; 0 Other;
Query Match 22.7%; Score 35; DB 13; Length 1797;
Best Local Similarity 56.5%; Pred. No. 20;
Matches 65; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 2 GGGCGAGCTGTATCTCGCTCATCTGCGAGTGGCGGCGGAGCTGTATCTGCTC 61
Db 597 GGGCGAGCTGTATCTCGCTCATCTGCGAGTGGCGGCGGAGCTGTATCTGCTC 656
QY 62 ATCGTCAGTGGCGGCGGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGTGGCGG 116
Db 657 GCGTCTGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 711

XX	RESULT 40
XX	ADP24630/C
XX	ID ADP24630 standard; cDNA; 1797 BP.
XX	ADP24630;
XX	18-NOV-2004 (first entry)
XX	PRO polypeptide encoding cDNA SEQ ID NO:1808.
DE	98; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW	immunosuppressive; osteopathic; antidiabetic; dermatological;
KW	antiporiatic; antiallergic; antiaesthetic; hepatotropic; respiratory;
XX	gene therapy; immune system.
XX	Unidentified.
OS	
XX	MO2004041170-A2.
PN	
XX	21-MAY-2004.
PD	
XX	30-OCT-2003; 2003WO-US034312.
PF	
XX	01-NOV-2002; 2002US-0423394P.
PR	(GERTH) GENENTECH INC.
XX	
PA	Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT,
PI	Wu TD;
XX	
DR	WPI; 2004-419628/39.
XX	P-PsDB; ADP24631.
PT	New PRO polypeptides and polynucleotides, useful for treating e.g.
PT	erythemaecus, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT	renal diseases, or demyelinating diseases of the central or peripheral
PT	nervous system.
XX	
PS	Claim 1; SEQ ID NO 1808; 2940pp; English.
XX	
XX	The invention relates to a novel isolated nucleic acid and the PRO
XX	polypeptide encoded by it. A protein of the invention has
XX	antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
CC	osteopathic, antidiabetic, dermatological, antiporiatic, antiallergic,
CC	antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
CC	of the invention may have a use in gene therapy. The PRO polypeptide, its
CC	agonist, antagonist, or antibody that specifically binds to the
CC	polypeptide is useful for treating an immune related disorder such as
CC	systemic lupus erythematousus, rheumatoid arthritis, osteoarthritis,
CC	juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, a
CC	idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC	vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC	thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC	disease, a demyelinating disease of the central or peripheral nervous
CC	system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome
CC	a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC	disease, infectious or autoimmune chronic active hepatitis, primary
CC	biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC	inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC	disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC	disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC	disease, asthma, allergic rhinitis, atopic dermatitis, food
CC	hypersensitivity, urticaria, an immunologic disease of the lung,
CC	eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC	pneumonitis, a transplantation associated disease, graft rejection or
CC	graft-versus-host disease. The present sequence encodes a PRO protein of
CC	the invention.
XX	
XX	Sequence 1797 BP; 263 A; 645 C; 552 G; 337 T; 0 U; 0 Other;
SQ	
XX	
XX	Query March 22 74; Score 35; DB 13; Length 1797;
XX	Beet Local Similarity 56.54; Pred. No. 20;

Matches	65;	Conservative	0;	Mismatches	50;	Indels	0;	Gaps	0
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Oy	39	GGCCGAGACTGTGTCATCTCGCTCATCTGTCAGTGGCGCGCCGCACTCGACATGAGCG	98
Db	711	GGCCGAGAGCGCGCGAGTCCGCGACCGCGCACCCAGCGCGCCGACGAGAGCGCAGG	652
Oy	99	AGATGACCAAGCTCCGCGCGCGGACTGCAGATGAGCGATGACCGAGCTCCGGCC	153
Db	651	TCCTGCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	597

RESULT 41
AA518438
AA518438 standard; DNA; 1681 BP.
XX
AC
AA518438;
XX
DT
12-MAR-2002 (first entry)
XX
DE
Contig 115 DNA encoding S. narbonensis polyketide synthase.
XX
XX
Narbonolide polyketide synthase; PKS; narbomycin modification enzyme;
KW
erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethylmycin;
XX
agriculture; ds.
XX
Streptomyces narbonensis.
OS
US6303767-B1.
PN
16-OCT-2001.
PD
XX
PF
05-NOV-1999; 99US-00434288.
XX
PR
05-NOV-1998; 98US-0107093P.
PR
27-MAY-1999; 99US-00320878.
XX
PA
(KOSA-) KOSAN BIOSCIENCES INC.
P1
Betlach MC, McDaniel R;
DR
WPI; 2002-065495/09.
PT
Nucleic acids encoding narbonolide polyketide synthases from Streptomyces
PT
narbonensis, useful for the recombinant production of polyketides, e.g.
narbomycin.
PS
Claim 1; Col 18; 24pp; English.
XX
XX
CC
The present invention relates to recombinant DNA vectors (cosmids) that
CC
encode for the narbonolide polyketide synthase (PKS) enzyme and various
CC
narbomycin modification enzymes from Streptomyces narbonensis. The
CC
recombinant DNA vectors can be used to produce recombinant ketide
CC
synthases and a variety of different polyketides (e.g. erythromycin,
CC
rapamycin, tylosin, narbomycin, picromycin, methylmycin and
CC
neomethylmycin) for use in agriculture, medicine and health. The
CC
recombinant vectors may be used to produce polyketides in relatively high
CC
Yields. AA518432-AA518443 represent contig DNA sequences that encode for
CC
S. narbonensis PKS enzymes
XX
XX
Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;

Qy	1	CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCCGGGCGCGAGCTGTCATCTCGCT	60
Db	424	CTGGCGCGCGCTCTCAGCGGCTCAACCGCGGCTCGCGCGCGCGCTTCGGTCCGC	483
Oy	61	CATGTCAGTCCGCGCGCGCGCGCGAGTCCAGCATGAGCGAGTACCACTCCGCGCG	118
Db	484	CGCGCGAGGCGCGCGCGCGAGCGGACCGCGCGAGAGAGGACCTTGGCGCGCGCG	541

Query Match	22.6%;	Score 34.8;	DB 6;	Length 1681;
Best Local Similarity	55.9%;	Pred. No. 22;		
Matches	66;	Conservative	0;	Mismatches 52;
				Indels 0;
				Gaps 0

RESULT 42
AAS18438/c
ID AAS18438 standard; DNA; 1681 BP.
XX
AC AAS18438;
XX
DT 12-MAR-2002 (first entry)
XX
DE Contig 115 DNA encoding S. narbonensis polyketide synthase.
XX
KW Narbonolide polyketide synthase; PKS; narbomycin modification enzyme;
KM erythromycin; rapamycin; tylosin; picromycin; methylmycin; neomethylmycin;
XX agriculture; ds.
OS Streptomyces narbonensis.
XX
PN US6303767-B1.
XX
PD 16-OCT-2001.
XX
PF 05-NOV-1999; 99US-00434288.
XX
PR 05-NOV-1998; 98US-0107093P.
XX
PR 27-MAY-1999; 99US-00320876.
XX
PA (KOSA-) KOSAN BIOSCIENCES INC.
XX
PI Belach MC, Medaniel R;
XX
DR WPI; 2002-065495/09.
XX
PT Nucleic acids encoding narbonolide polyketide synthases from Streptomyces
XX narbonensis, useful for the recombinant production of polyketides, e.g.
XX narbomycin.
XX
PS Claim 1; Col 18; 24pp; English.
XX
CC The present invention relates to recombinant DNA vectors (cosmids) that
XX encode for the narbonolide polyketide synthase (PKS) enzyme and various
XX narbomycin modification enzymes from Streptomyces narbonensis. The
XX recombinant DNA vectors can be used to produce recombinant ketide
XX synthases and a variety of different polyketides (e.g. erythromycin,
XX rapamycin, tylosin, narbomycin, picromycin, methylmycin and
XX neomethylmycin) for use in agriculture, medicine and health. The
XX recombinant vectors may be used to produce polyketides in relatively high
XX yields. AAS18432-AAS18443 represent contig DNA sequences that encode for
XX S. narbonensis PKS enzymes
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;
XX
Query Match 22.6%; Score 34.8; DB 6; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
XX
QY 37 GCGGCGGAGCTGCTCATCTCGCTCATGTCGAGTCGCGCGCGCGGCTGACGATGAG 96
XX
DB 541 GCGCGCGCGCGAGCTCTCTCCGCTGCGCGGCTGCGCGCGCGCGCTGCGCGCGC 482
XX
QY 97 CGAGATGACGAGCTCGCGCGCGCGGCTGACGATGAGCGAGTACGAGCTCGCGCGC 154
XX
DB 481 CGACCGGAGCGCGCGCGCGCGCGGCTGAGCGCGCGCGCGCGCGCGCGCGCGC 424
XX
RESULT 43
ADL91894
XX
AC ADL91894 standard; DNA; 1681 BP.
XX
ADL91894;
XX
DT 20-MAY-2004 (first entry)
XX
DE Streptomyces narbonolide polyketide synthase coding sequence #7.

XX
KW narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;
XX medical application; industrial application; ds.
XX
OS Streptomyces narbonensis.
XX
PN US2003194784-A1.
XX
PD 16-OCT-2003.
XX
PF 15-OCT-2002; 2002US-00271889.
XX
PR 17-APR-2001; 2001US-00836821.
XX
PR 18-MAY-2001; 2001US-00860846.
XX
PR 18-MAY-2001; 2001US-00861289.
XX
PA (SHER/) SHERMAN D H.
XX
PA (LIU/) LIU H.
XX
PA (XUEY/) XUE Y.
XX
PA (ZHAO/) ZHAO L.
XX
PI Sherman DH, Liu H, Xue Y, Zhao L;
XX
DR WPI; 2004-119267/12.
XX
PT New isolated nucleic acid comprising a narbonolide polyketide synthase
XX gene from Streptomyces narbonensis, useful for providing a
XX polyhydroxyalkanoate monomer for medical and industrial applications.
XX
PS Claim 1; SEQ ID NO 7; 362pp; English.
XX
CC The invention comprises coding sequences for the narbonolide polyketide
XX synthase gene from Streptomyces narbonensis. The DNA sequence of the
XX invention are useful for providing polyhydroxyalkanoate monomer for
XX medical and industrial applications. The present DNA sequence represents
XX a Streptomyces narbonensis narbonolide polyketide synthase coding
XX sequence of the invention.
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;
XX
Query Match 22.6%; Score 34.8; DB 12; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
XX
QY 1 CGGCGGAGCTGCTCATCTCGCTCATGTCGAGTCGCGCGCGCGGCTGATCTCGCT 60
XX
DB 424 CTGCGCGCGCTGCTCAAGCGGCTCAACCGCGGCTGCGCGCGCGCTCGGTCGCGC 483
XX
QY 61 CATGTCGAGTCGCGCGCGCGCGGCTGACGATGAGCGAGTACGAGCTCGCGCGC 118
XX
DB 484 CGCGCGAGGCGCGCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 541
XX
RESULT 44
ADL91894/c
XX
ID ADL91894 standard; DNA; 1681 BP.
XX
AC ADL91894;
XX
DT 20-MAY-2004 (first entry)
XX
DE Streptomyces narbonolide polyketide synthase coding sequence #7.
XX
KW narbonolide polyketide synthase gene; polyhydroxyalkanoate monomer;
XX medical application; industrial application; ds.
XX
OS Streptomyces narbonensis.
XX
PN US2003194784-A1.
XX
PD 16-OCT-2003.
XX
PF 15-OCT-2002; 2002US-00271889.

```
XX 17-APR-2001; 2001US-00836821.
PR 18-MAY-2001; 2001US-00860846.
PR 18-MAY-2001; 2001US-00861289.
XX
XX (SHER/) SHERMAN D H.
PA (LIU/) LIU H.
PA (XUEY/) XUE Y.
PA (ZHAO/) ZHAO L.
PI Sherman DH, Liu H, Xue Y, Zhao L;
XX
XX WPI; 2004-119267/12.
XX
PT New isolated nucleic acid comprising a narbonolide polyketide synthase
PT gene from Streptomyces narbonensis, useful for providing a
PT polyhydroxyalkanoate monomer for medical and industrial applications.
XX
PS Claim 1; SEQ ID NO 7; 362pp; English.
XX
CC The invention comprises coding sequences for the narbonolide polyketide
CC synthase gene from Streptomyces narbonensis. The DNA sequence of the
CC invention are useful for providing polyhydroxyalkanoate monomer for
CC medical and industrial applications. The present DNA sequence represents
CC a Streptomyces narbonensis narbonolide polyketide synthase coding
CC sequence of the invention.
XX
SQ Sequence 1681 BP; 231 A; 672 C; 580 G; 198 T; 0 U; 0 Other;
Query Match 22.6%; Score 34.8; DB 12; Length 1681;
Best Local Similarity 55.9%; Pred. No. 22;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
OY 37 GCGGCCGAGCTGTCATCTCTGCTCATGTGAGTGGCGCGCCGACTGAGCGATGAG 96
Db 541 GCCCCCGCCGCAAGTCTCTCCGCTGCGCGGTCCTCGCGCGCGCCCTGCGCGCGC 482
OY 97 CGAGATGACGAGCTCGCGCGCGCGCGAGTGAAGAGATGACGAGCTCGCGCGC 154
Db 481 CGACCGGAGCGCGCGCGCGCGCGAGCCGCGGAGCGCGCTGAGCAGCGCGCGCAG 424
RESULT 45
AAS59803
ID AAS59803 standard; DNA; 1498 BP.
XX
XX AAS59803;
AC
XX
XX 13-FEB-2002 (first entry)
DT
XX
XX Propionibacterium acnes immunogenic protein encoding DNA #298.
DE
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
XX uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
XX inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
XX dermatological; osteopathic; neuroprotectant; ds.
XX
XX Propionibacterium acnes.
OS
XX
XX W0200181581-A2.
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-US012865.
XX
XX 21-APR-2000; 2000US-0199047P.
XX 02-JUN-2000; 2000US-0208841P.
XX 07-JUL-2000; 2000US-0216747P.
XX
XX (CORI-) CORIYA CORP.
XX
XX Skeiky YAM, Persing DH, Mitcham JU, Wang SS, Bhatia A;
XX L'maisonneuve J, Zhang Y, Jen S, Carter D;
```

```
XX
XX WPI; 2001-616774/71.
DR
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris.
XX
XX Claim 1; SEQ ID NO 298; 1069pp; English.
XX
XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
XX Propionibacterium acnes immunogenic polypeptides. The proteins and their
XX associated DNA sequences are used in the treatment, prevention and
XX diagnosis of medical conditions caused by P. acnes. The disorders include
XX SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
XX osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in
XX infections of bone, joints and the central nervous system, however it is
XX particularly involved in the inflammatory lesions associated with acne
XX vulgaris. A method for detecting the presence or absence of P. acnes in a
XX patient comprises contacting a sample with a binding agent that binds to
XX the proteins of the invention and determining the amount of bound protein
XX in the sample. The polypeptides may be used as antigens in the production
XX of antibodies specific for P. acnes proteins. These antibodies can be
XX used to downregulate expression and activity of P. acnes polypeptides and
XX therefore treat P. acnes infections. The antibodies may also be used as
XX diagnostic agents for determining P. acnes presence, for example, by
XX enzyme linked immunosorbent assay (ELISA). This sequence encodes the
XX polypeptides shown in AAU67430-AAU67444 and AAU68011-AAU68015. Note: The
XX sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 1498 BP; 286 A; 458 C; 450 G; 301 T; 0 U; 3 Other;
Query Match 22.5%; Score 34.6; DB 4; Length 1498;
Best Local Similarity 56.6%; Pred. No. 25;
Matches 64; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
OY 30 CGATCGCGCGCGCGAGCTGTCATCTCGCTCATGTGAGTGGCGCGCGCGAGCTGCA 89
Db 696 CCACTCGCGAGCTGGCGCGCGATCCGCTCTGCTCTCACTTACCTATCACCACCAACC 755
OY 90 CGATGAGGAGATGACGAGCTCGCGCGCGCGAGTGAAGATGAGCGAGATGAC 142
Db 756 TGGTGAAGAGAGAGACCCGTAACCGCGCGCGAGCTGCTGTCGAGAGCTGTGAC 808
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Search completed: April 8, 2005, 23:27:00
Job time : 442 secs

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OM nucleic - nucleic search, using sw model.

Run on: April 8, 2005, 21:45:05 ; Search time 1885 Seconds
(without alignments)
3958.675 Million cell updates/sec

Title: US-09-887-194a-13

Perfect score: 154

Sequence: 1 cggcgcgagctgcgtcatctc.....gagatgacagctccgcgcg 154

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_bcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	154	100.0	154	6	AX367128 Sequence
2	154	100.0	154	6	AX367128 Sequence
3	154	100.0	154	6	AX392336 Sequence
4	154	100.0	154	6	AX392336 Sequence
5	112	72.7	4974	6	AX353724 Sequence
6	112	72.7	4974	6	AX353724 Sequence
7	82.8	53.8	6611	6	AX392337 Sequence
8	82.8	53.8	6611	6	AX392337 Sequence
9	81	52.6	963	6	AX367144 Sequence
10	81	52.6	963	6	AX367144 Sequence
11	80	51.9	80	6	AX367127 Sequence
12	80	51.9	80	6	AX367127 Sequence
13	80	51.9	80	6	AX392335 Sequence
14	80	51.9	80	6	AX392335 Sequence
15	80	51.9	92	6	AX367129 Sequence
16	80	51.9	92	6	AX367129 Sequence
17	45.8	29.7	1717	6	AX367139 Sequence
18	45.8	29.7	1717	6	AX367139 Sequence
19	41.8	27.1	13802	1	STB579650 Streptomy

C	20	41.8	27.1	13802	1	STB579650
C	21	38.6	25.1	110000	1	BX571966_08
C	22	38.6	25.1	110000	1	BX571966_08
C	23	38.2	24.8	10348	1	AE004846
C	24	38.2	24.8	10348	1	AE004846
C	25	38.2	24.7	301925	1	AP005046
C	26	38	24.7	301925	1	AP005046
C	27	37	24.0	148829	8	AC134925
C	28	37	24.0	148829	8	AC134925
C	29	36.8	23.9	110000	1	AP006618_59
C	30	36.8	23.9	110000	1	AP006618_59
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C	32	36.6	23.8	110000	1	AE016822_14
C	33	36.6	23.8	349315	1	BX572593
C	34	36.6	23.8	349315	1	BX572593
C	35	36.4	23.6	674	8	AK063727
C	36	36.4	23.6	674	8	AK063727
C	37	36.4	23.6	133449	8	AC107207
C	38	36.4	23.6	133449	8	AC107207
C	39	36.4	23.6	150743	8	AC133450
C	40	36.4	23.6	150743	8	AC133450
C	41	36.2	23.5	8973	1	AY081837
C	42	36.2	23.5	8973	1	AY081837
C	43	36.2	23.5	123169	9	AC008771
C	44	36.2	23.5	123169	9	AC008771
C	45	36.2	23.5	126052	9	AC018764
C	46	36.2	23.5	126052	9	AC018764
C	47	36.2	23.5	298550	1	AP005961
C	48	36.2	23.5	298550	1	AP005961
C	49	36	23.4	129647	8	AC097280
C	50	36	23.4	129647	8	AC097280
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C	52	36	23.4	190050	1	AL646059
C	53	36	23.4	344805	1	BX640434
C	54	36	23.4	344805	1	BX640434
C	55	36	23.4	348074	1	BX640449
C	56	36	23.4	348074	1	BX640449
C	57	35.8	23.2	1044	8	AK108311
C	58	35.8	23.2	1044	8	AK108311
C	59	35.8	23.2	1102	8	HVMB2
C	60	35.8	23.2	1102	8	HVMB2
C	61	35.8	23.2	180186	8	AP003104
C	62	35.8	23.2	180186	8	AP003104
C	63	35.8	23.2	283100	1	SCO939110
C	64	35.8	23.2	283100	1	SCO939110
C	65	35.6	23.1	103788	8	AP004747
C	66	35.6	23.1	103788	8	AP004747
C	67	35.6	23.1	119290	8	AP005300
C	68	35.6	23.1	119290	8	AP005300
C	69	35.6	23.1	278492	1	BX248347
C	70	35.6	23.1	278492	1	BX248347
C	71	35.6	23.1	302178	1	AE016918
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C	75	35.2	22.9	325483	1	AP005050
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C	77	35	22.7	1020	9	AB078417
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C	80	35	22.7	1797	9	AF438313
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C	82	35	22.7	223542	9	AC006515
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C	84	35	22.7	302174	1	AE017241
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AJ579650 Streptomy
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AP005046 Streptomy
AP005046 Streptomy
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Continuation) of o
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AK108311 Oryza sat
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AP005050 Streptomy
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AC006515 Homo sapi
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AP005043 Streptomy

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ALIGNMENTS

RESULT 1
 AX367128
 LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
 DEFINITION Sequence 13 from Patent WO0200904.
 ACCESSION AX367128
 VERSION AX367128.1 GI:18855329
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE
 AUTHORS Glaesman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L. and Nichols, S.E.
 TITLE Recombinant constructs and their use in reducing gene expression
 JOURNAL E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES
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 1.154
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="ELVISLIVES complementary region of PKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
 DB 1 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
 QY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 120
 DB 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 120
 QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 154
 DB 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 154

RESULT 2

AX367128/c
 LOCUS AX367128 154 bp DNA linear PAT 16-FEB-2002
 DEFINITION Sequence 13 from Patent WO0200904.
 ACCESSION AX367128
 VERSION AX367128.1 GI:18855329
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE

AUTHORS Glaesman, K.F., Gordon-Kamm, W.J., Kinney, A.J., Lowe, K., Stecca, K.L. and Nichols, S.E.
 TITLE Recombinant constructs and their use in reducing gene expression
 JOURNAL E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED INTERNATIONAL, INC. (US)

FEATURES
 Location/Qualifiers

source

1.154
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="ELVISLIVES complementary region of PKS133"

Query Match 100.0%; Score 154; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
 DB 154 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 95
 QY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 120
 DB 94 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 35
 QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 154
 DB 34 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 1

RESULT 3
 AX392336
 LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 25 from Patent WO0216565.
 ACCESSION AX392336
 VERSION AX392336.1 GI:19700689
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE
 AUTHORS Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
 TITLE Nucleotide sequences of a new class of diverged delta-9
 JOURNAL stearoyl-acp desaturase genes
 Patent: WO 0216565-A 25 28-FEB-2002;
 E. I. du Pont de Nemours and Company (US)

FEATURES
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 1.154
 /organism="synthetic construct"
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 /db_xref="taxon:32630"
 /note="ELVISLIVES complementary region of PKS133"

ORIGIN

Query Match 100.0%; Score 154; DB 6; Length 154;
 Best Local Similarity 100.0%; Pred. No. 1.1e-19;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
 DB 1 CGGCCGAGCTGGTATCTCGTCTCATGTCGAGTGGCGCGGAGCTGTCATCTCGCT 60
 QY 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 120
 DB 61 CATCGTCGAGTCGGCGCGCGCGGAGCTCGACGATGAGCGAGATGACCAAGCTCCGGCCGCG 120
 QY 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 154
 DB 121 ACTCGACGATGAGCGAGATGACCAAGCTCCGGCCG 154

RESULT 4

AX392336/c
 LOCUS AX392336 154 bp DNA linear PAT 23-MAR-2002
 DEFINITION Sequence 25 from Patent WO0216565.
 ACCESSION AX392336
 VERSION AX392336.1 GI:19700689
 KEYWORDS
 SOURCE synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL stearyl- α -cp desaturase genes
E. I. du Pont de Nemours and Company (US)
LOCATION/Qualifiers
1. .154
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS133"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1,1e-19;
Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
Db 154 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 95
Qy 61 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCCGGCGCG 120
Db 94 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCCGGCGCG 35
Qy 121 ACTCGACGATGAGCGAGATGACAGCTCCGGCG 154
Db 34 ACTCGACGATGAGCGAGATGACAGCTCCGGCG 1

RESULT 5
AX353724 4974 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 17 from Patent EPI174510.
ACCESSION AX353724
VERSION AX353724.1 GI:18618779
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Allen, S.M., Butler, K.H., Carlson, T.J. and Ilag, L.L.
TITLE Plasmidial phosphoglucomutase genes
JOURNAL Patent: EP 1174510-A 17 23-JAN-2002;
E. I. du Pont de Nemours and Company (US)
LOCATION/Qualifiers
1. .4974
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/db_xref="taxon:32630"

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Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
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Qy 61 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCC 112
Db 4923 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCC 4974

RESULT 6
AX353724 4974 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 17 from Patent EPI174510.
ACCESSION AX353724

VERSION AX353724.1 GI:18618779
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS Allen, S.M., Butler, K.H., Carlson, T.J. and Ilag, L.L.
TITLE Plasmidial phosphoglucomutase genes
JOURNAL Patent: EP 1174510-A 17 23-JAN-2002;
E. I. du Pont de Nemours and Company (US)
LOCATION/Qualifiers
1. .4974
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

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Query Match 72.7%; Score 112; DB 6; Length 4974;
Best Local Similarity 100.0%; Pred. No. 5e-12;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 102
Db 4974 GAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 4915
Qy 103 GACGAGCTCCGCGCGGAGTCGACGATGAGATGACAGCTCCGGCGCG 154
Db 4914 GACGAGCTCCGCGCGGAGTCGACGATGAGATGACAGCTCCGGCGCG 4863

RESULT 7
AX392337 6611 bp DNA linear PAT 23-MAR-2002
LOCUS
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION AX392337
VERSION AX392337.1 GI:19700690
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
AUTHORS Booth, J.R., Cahoon, R.E., Hitz, W.D., Kinney, A.J. and Yadav, N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL stearyl- α -cp desaturase genes
E. I. du Pont de Nemours and Company (US)
LOCATION/Qualifiers
1. .6611
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Plasmid pBS68"

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Query Match 53.8%; Score 82.8; DB 6; Length 6611;
Best Local Similarity 97.7%; Pred. No. 1.6e-06;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 60
Db 5348 CGGCGGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGGAGCTGTCATCTCGCT 5407
Qy 61 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCC 86
Db 5408 CATGTCGAGTCGGCGCGGCGGAGTCGACGATGAGATGACAGCTCC 5433

RESULT 8
AX392337 6611 bp DNA linear PAT 23-MAR-2002
LOCUS
DEFINITION Sequence 26 from Patent WO0216565.
ACCESSION AX392337
VERSION AX392337.1 GI:19700690

KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Booch,J.R., Cahoon,R.E., Hltz,W.D., Kinney,A.J. and Yadav,N.S.
TITLE Nucleotide sequences of a new class of diverged delta-9
JOURNAL Patent: WO 0216565-A 26 28-FEB-2002;
E. I. du Pont de Nemours and Company (US)
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/note="Plasmid pBS68"
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Best Local Similarity 97.7%; Pred. No. 1.6e-06;
Matches 84; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 69 AGTCGCGCGCCGCACTCGACGATGAGGAGATGACCACTCCGCGCCGCGACTCGACG 128
DB 5433 ACTCAGCGCGCCGCGCACTCGACGATGAGGAGATGACCACTCCGCGCCGCGACTCGACG 5374
QY 129 ATGACGAGATGACGAGCTCCGCGCG 154
DB 5373 ATGACGAGATGACGAGCTCCGCGCG 5348
RESULT 9
AX367144 963 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 29 from Patent WO0200904.
ACCESSION AX367144
VERSION AX367144.1 GI:18855345
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 29 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
FEATURES
source
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/organism="synthetic construct"
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/note="ELVISLIVES complementary region of pKS149"
ORIGIN
Query Match 52.6%; Score 81; DB 6; Length 963;
Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 74 GCGCGCGCGCACTCGACGATGAGGAGATGACCACTCCGCGCCGCGACTCGACGATGAG 133
DB 883 GCGCGCGCGCACTCGACGATGAGGAGATGACCACTCCGCGCCGCGACTCGACGATGAG 942
QY 134 CGAGTGAACGAGCTCCGCGCG 154
DB 943 CGAGTGAACGAGCTCCGCGCG 963
RESULT 10
AX367144 963 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 29 from Patent WO0200904.

ACCESSION AX367144
VERSION AX367144.1 GI:18855345
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 29 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
FEATURES
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/note="ELVISLIVES complementary region of pKS149"
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Best Local Similarity 100.0%; Pred. No. 5.1e-06;
Matches 81; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGCGGAGAGTGGTCACTCGCTCATCTGAGTGGCGCGCGAGCTGTCATCTCGCT 60
DB 963 CGGCGGAGAGTGGTCACTCGCTCATCTGAGTGGCGCGCGAGCTGTCATCTCGCT 904
QY 61 CATGTCGAGTCGGCGCGCG 81
DB 903 CATGTCGAGTCGGCGCGCG 883
RESULT 11
AX367127 80 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 12 from Patent WO0200904.
ACCESSION AX367127
VERSION AX367127.1 GI:18855328
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 0200904-A 12 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
FEATURES
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/note="ELVISLIVES complementary region of pKS106 and pKS124"
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Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 38 CGGCGGAGAGTGGTCACTCGCTCATCTGAGTGGCGCGCGAGCTGTCATCTGAGC 97
DB 1 CGGCGGAGAGTGGTCACTCGCTCATCTGAGTGGCGCGCGAGCTGTCATCTGAGC 60
QY 98 GAGATGACGAGCTCCGCGCG 117
DB 61 GAGATGACGAGCTCCGCGCG 80

RESULT 12
AX367127/c 80 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 12 from Patent WO0200904.
ACCESSION AX367127
VERSION AX367127.1 GI:18855328
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS106 and pKS124"

ORIGIN
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 97
DB 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 21
QY 98 GAGATGACCACTCCGGCCG 117
DB 20 GAGATGACCACTCCGGCCG 1

RESULT 13
AX392335 80 bp DNA linear PAT 23-MAR-2002
LOCUS
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION AX392335
VERSION AX392335.1 GI:19700688
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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1. .80
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES complementary region of pKS106 and pKS124"

ORIGIN
Query Match 51.9%; Score 80; DB 6; Length 80;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 97
DB 1 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 60
QY 98 GAGATGACCACTCCGGCCG 117

DB 61 GAGATGACCACTCCGGCCG 80
RESULT 14
AX392335 80 bp DNA linear PAT 23-MAR-2002
LOCUS
DEFINITION Sequence 24 from Patent WO0216565.
ACCESSION AX392335
VERSION AX392335.1 GI:19700688
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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/note="ELVISLIVES complementary region of pKS106 and pKS124"

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Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 97
DB 80 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 21
QY 98 GAGATGACCACTCCGGCCG 117
DB 20 GAGATGACCACTCCGGCCG 1

RESULT 15
AX367129 92 bp DNA linear PAT 16-FEB-2002
LOCUS
DEFINITION Sequence 14 from Patent WO0200904.
ACCESSION AX367129
VERSION AX367129.1 GI:18855330
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1. .92
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"

ORIGIN
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTCGCTCATCTCGAGTCGGCGCGCGGACTCGACGATGAGC 97

Db 7 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGCCGCACTGCAGATGAGC 66
QY 98 GAGATGACCACTCCGGCCG 117
Db 67 GAGATGACCACTCCGGCCG 86

RESULT 16
AX367129/c
LOCUS AX367129 92 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 14 from Patent WO200904.
ACCESSION AX367129
VERSION AX367129.1 GI:18855330
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1
Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 020904-A 14 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1. .92
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="ELVISLIVES PCR primer"

ORIGIN
Query Match 51.9%; Score 80; DB 6; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.2e-05;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGCCGCACTGCAGATGAGC 97
Db 86 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGCCGCACTGCAGATGAGC 27

QY 98 GAGATGACCACTCCGGCCG 117
Db 26 GAGATGACCACTCCGGCCG 7

RESULT 17
AX367139
LOCUS AX367139 1717 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 24 from Patent WO200904.
ACCESSION AX367139
VERSION AX367139.1 GI:18855340
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1
Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 020904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
FEATURES
source Location/Qualifiers
1. .1717
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Matches 47; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DEFINITION Sequence 24 from Patent WO200904.
ACCESSION AX367139
VERSION AX367139.1 GI:18855340
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1
Glassman,K.F., Gordon-Kamm,W.J., Kinney,A.J., Lowe,K., Stecca,K.L.
and Nichols,S.E.
TITLE Recombinant constructs and their use in reducing gene expression
JOURNAL Patent: WO 020904-A 24 03-JAN-2002;
E. I. du Pont de Nemours and Company (US) ; PIONEER HI-BRED
INTERNATIONAL, INC. (US)
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DEFINITION Streptomyces tenebrarius tobramycin biosynthetic gene cluster,
strain ATCC 17920.
ACCESSION A579650
VERSION A579650.1 GI:4554448
KEYWORDS 2-deoxy-scyllio-inosose aminotransferase; 2-deoxy-scyllio-inosose
synthase; carbanoyltransferase; dehydrogenase; glycosyltransferase;
ORF1; ORF2; ORF3; tacA gene; tacD gene; tbmA gene; tbmB gene; tbmC
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ORGANISM Streptomyces tenebrarius
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AUTHORS 1
Kharel,M.K., Baner,D.B., Lee,H.C., Liou,K., Woo,J.S., Kim,B.G. and
Sohng,J.K.
TITLE Isolation and characterization of the tobramycin biosynthetic gene
JOURNAL cluster from Streptomyces tenebrarius
PUBMED FEWS Microbiol. Lett. 230 (2), 185-190 (2004)
14757238
REFERENCE 2
Kharel,M.K., Lee,H.C., Liou,K., Woo,J.S. and Sohng,J.K.
AUTHORS An approach for cloning biosynthetic genes of 2-deoxystreptamine
TITLE containing aminocyclitol antibiotics: isolation of biosynthetic
JOURNAL gene cluster of tobramycin from S. tenebrarius
REFERENCE Unpublished
AUTHORS 3 (bases 1 to 13802)
Sohng,J.K.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Sohng J.K., Chemistry, Sun Moon University,
100 Kalsanri, Tangleongmyun, Asan si, Chungchungnamdo, 336-708,

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100 Kalsanri, Tangjeongmyun, Asan si, Chungchungnamdo, 336-708,
SOUTH KOREA

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Db 8012 CCCGATCTGATGTCGCCGAGCCCTCGCCGGGAGGTCGCCGCACTGCTGCGCGCC 8071
Qy 80 GCCGACTCGACGATGAGAGATGACGAGCTCCGGCCGC 118
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RESULT 25														
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LOCUS Streptomyces avermitilis genomic DNA, complete genome, section 26/30.														
ACCESSION AP005046 BA000030														

KEYWORDS	AP005046.1 GI:29609904
SOURCE	Streptomyces avermitilis MA-4680
ORGANISM	Streptomyces avermitilis MA-4680
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
AUTHORS	1 Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M.
TITLE	Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
MEDLINE	21477403
PUBMED	11572948
REFERENCE	2 Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S., Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis Nat. Biotechnol. 21 (5), 526-531 (2003)
AUTHORS	3 (bases 1 to 301925) Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, N., Director-General of Biotechnology Center, Shiba, T., Sakaki, Y. and Hattori, M.
REFERENCE	Direct Submission Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shiba-ku, Tokyo 151-0066, Japan (E-mail:biocentre.go.jp, URL:http://www.bio.nite.go.jp/). Tel.:81-3-3481-1933, Fax:81-3-3481-8424)
AUTHORS	This work was done in collaboration with Hano Ikeda(*1), Jun Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Shinose(*3), Hiroyuki Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Osone(*4), Norihiro Kuehida(*4), Hisaaki Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahito Hattori(*1,*7) and Satoshi Omura(*1,*3).
COMMENT	Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa. *1 Kitasato Institute for Life Sciences, Kitasato University *2 National Institute of Infectious Diseases *3 The Kitasato Institute *4 National Institute of Technology and Evaluation *5 School of Science, Kitasato University *6 Institute of Medical Science, University of Tokyo *7 RIKEN, Genomic Sciences Center Following url is also available. http://avermitilis.jb.kitasato-u.ac.jp. Location/Qualifiers 1..301925 /organism="Streptomyces avermitilis MA-4680" /mol_type="genomic DNA" /strain="MA-4680" /db_xref="taxon:227882" /note="This strain is also named as strain: ATCC 31267, NCIMB 12804 or NRRL B165.-synonym: Streptomyces avermectinatus" 37..831 /note="SAV6242" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="BAC73953.1" /db_xref="GI:29609905" /translation="MEGTREGDSSLAEGRLAEGSSLDLDEHTGRCAPRLVWRE EVARTRARAFADWYTWGRPVGRFGVNDLSLVGLAPAAHAGNTGMEFGSGDVL YALHVGASRAIVASDDGDELTGAVITSPVCAKPAKPTPERDCTPMLYREL ELRLPTLRVVVGLFPAQOALLPALAEGWVPPRPAPAFAGVATVTRPSAGPPASL DIVGCFHVQSQNTFTGRLLTPMLRDVLTAAEAGLPTLPDAGGYA"

VERSION

AP005046.1 GI:29609904

KEYWORDS

Streptomyces avermitilis MA-4680

SOURCE

Streptomyces avermitilis MA-4680

ORGANISM

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE

Ikeda, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M.

AUTHORS

Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites

TITLE

Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)

JOURNAL

21477403

MEDLINE

11572948

PUBMED

2

REFERENCE

Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S.

AUTHORS

Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis

TITLE

Natl. Biotechnol. 21 (5), 526-531 (2003)

JOURNAL

22608306

MEDLINE

12692562

PUBMED

3 (bases 1 to 301925)

REFERENCE

Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y. and Hattori, M.

AUTHORS

Direct Submission

TITLE

Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishinara, Shibuya-ku, Tokyo 151-0066, Japan

JOURNAL

E-mail: biocentre.go.jp, URL: http://www.bio.nite.go.jp/, Tel: 81-3-3481-1933, Fax: 81-3-3481-8424

COMMENT

This work was done in collaboration with Haruo Ikeda (*1), Jun Ishikawa (*2), Akiharu Hanamoto (*3), Chigusa Takahashi (*3), Mayumi Shinose (*3), Hiroshi Horikawa (*4), Hidekazu Nakazawa (*4), Tomomi Osone (*4), Norihiro Kishida (*4), Hisashi Kikuchi (*4), Tadayoshi Shiba (*5), Yoshiyuki Sakaki (*6,*7), Masahira Hattori (*1,*7) and Satoshi Omura (*1,*3).

FEATURES

Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.

SOURCE

*1 Kitasato Institute for Life Sciences, Kitasato University

FEATURES

*2 National Institute of Infectious Diseases

FEATURES

*3 The Kitasato Institute

FEATURES

*4 National Institute of Technology and Evaluation

FEATURES

*5 School of Science, Kitasato University

FEATURES

*6 Institute of Medical Science, University of Tokyo

FEATURES

*7 RIKEN, Genomic Sciences Center

FEATURES

Following url is also available.

FEATURES

http://avermitilis.is.kitasato-u.ac.jp.

FEATURES

Location/Qualifiers

FEATURES

1..301925

FEATURES

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 Matches 65; Conservative 0; Mismatches 45; Indels 0; Gaps 0;

CDS

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QY 102 TGACCAAGTCGCGCGCGCGACTCGACGATGAGCGAGATACCAAGTCGCGG 151

Db 118310 TCGTGCTCCGTACTGCGACGCCCGGACGAGACCGCGCAACTGCTCGGG 118359

RESULT 26
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 26/30.
 ACCESSION AP005046 BA0000030
 VERSION AP005046.1 GI:29609904
 KEYWORDS
 Streptomyces avermitilis MA-4680

ORGANISM	Streptomyces avermitilis MA-4680
REFERENCE	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
AUTHORS	1 Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinoue, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y., and Hattori, M.
TITLE	Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
MEDLINE	21477403
PUBMED	11572948
REFERENCE	2
AUTHORS	Ikeda, H., Ishikawa, J., Hanamoto, A., Shinoue, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M., and Omura, S.
TITLE	Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
JOURNAL	Nat. Biotechnol. 21 (5), 526-531 (2003)
MEDLINE	22608306
PUBMED	12692562
REFERENCE	3 (bases 1 to 301925)
AUTHORS	Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C., Shinoue, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osone, T., Kikuchi, H., Shiba, T., Sakaki, Y., and Hattori, M.
TITLE	Direct Submission
JOURNAL	Submitted (29-MAR-2002) Director-General of Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail: bio@nitech.go.jp, URL: http://www.bio.nitech.go.jp/, Tel: 81-3-3481-1933, Fax: 81-3-3481-8424)
COMMENT	This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa(*2), Akihito Hanamoto(*3), Chigusa Takahashi(*3), Mayumi Osone(*4), Hiroshi Horikawa(*4), Hidekazu Nakazawa(*4), Tomomi Shiba(*5), Norihiro Kishida(*4), Hisashi Kikuchi(*4), Tadavoshi and Satochi Omura(*1,*3). Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa. *1 Kitasato Institute for Life Sciences, Kitasato University *2 National Institute of Infectious Diseases *3 The Kitasato Institute *4 National Institute of Technology and Evaluation *5 School of Science, Kitasato University *6 Institute of Medical Science, University of Tokyo *7 RIKEN, Genomic Sciences Center Following url is also available. http://avermitilis.kitasato-u.ac.jp.
FEATURES	Location/Qualifiers
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REFERENCE	Emharitoidaeae; Oryzaeae: Oryza.
AUTHORS	1 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K., Pal,A.K., Dalal,V., Batra,K., *McCombie,W.R., *Spiegel,L., *de la Bastide,M., *Zutavern,T., *Miller,S., *Nascimento,L., *Bailja,V., *Bell,M., *Miller,B., *Katzenberger,F., *Andrade,M.V., *Dike,S., *O'Shaughnessy,A., *Palmer,L., Galkwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
JOURNAL	Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone OSUNBa0041u17, complete sequence
REMARK	*Iita Akenberg Hazen Genome Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.
REFERENCE	2 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K., Singh,A., Pal,S., Sureshabu,K., Srivastava,S., Pal,A.K., Dalal,V., Galkwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
AUTHORS	Direct Submission
JOURNAL	Submitted (02-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, IBS Centre, New Delhi, Delhi 110012, India
REFERENCE	3 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Bhargava,A., Dixit,A., Swain,S.C., Batra,K., Singh,A., Pal,S., Sureshabu,K., Srivastava,S., Pal,A.K., Dalal,V., Galkwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
AUTHORS	Direct Submission
JOURNAL	Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, IBS Centre, New Delhi, Delhi 110012, India
REFERENCE	4 (bases 1 to 148829) Ghazi,I.A., Yadav,M., Dixit,R., Singh,A., Srivastava,S.K., Pal,A.K., Dalal,V., Batra,K., McCombie,W.R., Spiegel,L., de la Bastide,M., Zutavern,T., Muller,S., Nascimento,L., Bailja,V., Bell,M., Miller,B., Katzenberger,F., Andrade,M.V., Dike,S., O'Shaughnessy,A., Palmer,L., Galkwad,K., Sharma,T.R., Mohapatra,T. and Singh,N.K.
AUTHORS	Direct Submission
JOURNAL	Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, IBS Centre, New Delhi, Delhi 110012, India
COMMENT	On Mar 21, 2004 this sequence version replaced gi:28604233. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi Genome Center under the Ind-US collaboration. Clone OSUNBa0041u17 overlaps clone OSUNBa0007D07 from base 100381 to base 148829. The overlap is from base 1 to base 48448 on OSUNBa0007D07.
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misc_feature	/note="The assembly is covered by high quality sequences generated from a transposed plasmid subclone." 66330..66375
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REFERENCE	TITLE	AUTHORS
ORANISM	Oryza sativa (japonica cultivar-group)	
REFERENCE	Bukariyota Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.	
REFERENCE	1 (bases 1 to 148829)	
REFERENCE	Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., Pal, A.K., Datal, V., Barra, K., McCombie, W.R., Spiegel, L., *de la Bactie, M., Zutavern, T., Muller, S., Nascimento, L., Balija, V., *Bell, M., Miller, B., Katzenberger, F., Andrade, M.V., *Dike, S., *O'Shaughnessy, A., *Palmer, L., Galkwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.	
REFERENCE	Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone OSUNBa0041J17, complete sequence	
REFERENCE	Unpublished	
REFERENCE	*Iita Akenberg Hazen Genome Center, Cold Spring Harbor Laboratory 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA.	
REFERENCE	2 (bases 1 to 148829)	
REFERENCE	Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain, S.C., Barra, K., Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pal, A.K., Datal, V., Galkwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.	
REFERENCE	Direct Submission	
REFERENCE	Submitted (02-OCT-2002) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India	
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REFERENCE	Ghazi, I.A., Yadav, M., Bhargava, A., Dixit, A., Swain, S.C., Barra, K., Singh, A., Pal, S., Sureshbabu, K., Srivastava, S., Pal, A.K., Datal, V., Galkwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.	
REFERENCE	Direct Submission	
REFERENCE	Submitted (28-FEB-2003) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India	
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REFERENCE	Ghazi, I.A., Yadav, M., Dixit, R., Singh, A., Srivastava, S.K., Pal, A.K., Datal, V., Barra, K., McCombie, W.R., Spiegel, L., de la Bactie, M., Zutavern, T., Muller, S., Nascimento, L., Balija, V., Bell, M., Miller, B., Katzenberger, F., Andrade, M.V., Dike, S., O'Shaughnessy, A., Palmer, L., Galkwad, K., Sharma, T.R., Mohapatra, T. and Singh, N.K.	
REFERENCE	Direct Submission	
REFERENCE	Submitted (21-MAR-2004) IIRGS, NRC on Plant Biotechnology, Indian Agricultural Research Institute, LBS Centre, New Delhi, Delhi 110012, India	
REFERENCE	On Mar 21, 2004 this sequence version replaced gi:28604232. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. This BAC clone was sequenced to phase II by the National Research Centre on Plant Biotechnology, Indian Agricultural Research Institute, New Delhi and was completed to phase III by the Cold Spring Harbor Laboratory Genome Center under the Indo-US collaboration. Clone OSUNBa0041J17 overlaps clone OSUNBa0007D07 from base 100381 to base 148829. The overlap is from base 1 to base 4848 on OSUNBa0007D07.	
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RPAAGLYIIDLTHNVRGMDWVTGYAKLFNPROIRFEDIGRASGLPSRLTSP
DGKIRIPINEDAGSGOIEEYLSLYRGSGIOLHACGCRDIYSTEYGLRAALDPMPS
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EREQAAARESERLARAILASANEAVYCDAGVTHLNGAAMRI CABAPGKTFPAA
IATSPASELMSDDIVYATAGIPVQGLEAAVIRPSAALTDMVISAAPLVSGERT
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Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 298677 CGCATCTTCAGATGGCTGTGCGTGAACCATTCATGATCGGCTGCGCGCGCG 298736

Qy 82 CGACTCGACGATGACCGAGATGACCGAGCTCCGCGCCGACTCGACG 128
Db 298737 CACCTCGTCCGACCCCGAGCGCTCGACACGCGCGCGCGCGCGCG 298783

RESULT 34
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LOCUS Rhodopseudomonas palustris CGA009 complete genome; segment 1/16.
DEFINITION BX572593 BX571963
ACCESSION BX572593.1 GI:39652705
VERSION
KEYWORDS complete genomes.
SOURCE Rhodopseudomonas palustris CGA009
ORGANISM Rhodopseudomonas palustris CGA009
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiales; Rhodopseudomonas.
REFERENCE
1 (bases 1 to 349315)
Larimer, F.W., Chain, P., Hauser, L., Lamerdin, J., Malfatti, S., Do, L.,
Land, M.L., Pelletier, D.A., Beatty, J.T., Lang, A.S., Tabita, F.R.,
Gibson, J.L., Hanson, T.E., Bobst, C., Torres, J.L., Pares, C.,
Harrison, F.H., Gibson, J. and Harwood, C.S.
Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris
Nat. Biotechnol. 22 (1), 55-61 (2004)
TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
CONSTRM
TITLE
JOURNAL
Submitted (24-JUL-2003) Submitted on behalf of the Rhodopseudomonas
genome consortium, the DOE Joint Genome Institute, Production
Genomics Facility, 2800 Mitchell Drive, Walnut Creek, CA 94598,
USA, and the Genome Analysis Group, Oak Ridge National Laboratory,
1060 Commerce Park Drive, Oak Ridge, TN 37831, USA;
larimerf@ornl.gov
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Best Local Similarity 58.9%; Pred. No. 4.3e+02;
Matches 63; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

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Db 298783 CGGGGTGGCGCGCGGCTGTTCAGGCGCTGGGAGTGGAGTGGCGCGCGCGCGCG 298724

Qy 87 CGAGCATGACGACATGACACGACCTCCGCGCGCGCGCATGACGATGAG 133
Db 298723 AGCCGATCATGATATGTGTCTGACCGACGACCATCTTGAGATGCG 298677

RESULT 35
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LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-120-E01, full
DEFINITION insert sequence.
ACCESSION AK063727
VERSION AK063727.1 GI:32973745
KEYWORDS P11 CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.
1

REFERENCE
AUTHORS The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yanagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Oono,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J.,
Iweda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Kono,H., Miyazaki,A., Oosato,N., Oca,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M., and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
Science 301 (5631), 376-379 (2003)

TITLE japonica rice
JOURNAL MEDLINE 22752273
PUBMED 12869764

REFERENCE
AUTHORS 2 (bases 1 to 674)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hirooka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Iweda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kawagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Narikawa,R., Narikawa,R., Niihara,J., Niihara,K., Nomura,K.,
Nunaseki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,

Osato,N., Oca,Y., Oono,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yanagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S., and
Yoshimura,A.
Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28k full-length cDNA clones from japonica
rice.
URL: <http://cdna01.dna.affrc.go.jp/cDNA/>
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yanagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Oono,Y., Iida,Y.,
Fujimura,T., Iweda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Niihara,J., Niihara,K., Nomura,K., Oono,Y.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K., and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Kono,H., Kouda,M.,
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Oca,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A., and Hayashizaki,Y.
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FEATURES
source

ORIGIN
Query Match 23.8%; Score 36.4; DB 8; Length 674;
Best Local Similarity 58.2%; Pred. No. 1.5e+03;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 42 CGAGCTGTGCATCTGCTCATCTGCTGAGTGGCGCGCGCGCATGACGATGAGCGAGA 101
Db 175 CGGGTGGCGCGCGGCTGTTCAGGCGCTGGGAGTGGAGTGGCGCGCGCGCGCG 234

Qy 102 TGACCATCTCGCGCGCGCGCATGACGATGAGCGACGACCTCCGG 151
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LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:001-120-E01, full
DEFINITION insert sequence.
ACCESSION AK063727
VERSION AK063727.1 GI:32973745
KEYWORDS P11 CDNA; oligo-capping.
SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM
Oryza sativa (japonica cultivar-group)

REFERENCE
AUTHORS
1
The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA project Team, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ootomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nakikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Nishikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Kono, H., Miyazaki, A., Ootomo, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL
MEDLINE
22752273
12869764
2 (bases 1 to 674)

REFERENCE
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Maeda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, W., Nagata, T., Nakamura, M., Namiki, T., Nakikawa, R., Nishikura, J., Nishikura, M., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Ootomo, N., Ota, Y., Ootomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S., and Yoshimura, A.

TITLE
Direct Submission

JOURNAL
COMMENT
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@niae.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.
URL: http://cdna01.dna.affrc.go.jp/cDNA/NIAE_Rice_Full-length_cDNA_Project_Team_Kikuchi_S_Satoh_K_Nagata_T_Kawagashira_N_Doi_K_Kishimoto_N_Yazaki_J_Ishikawa_M_Yamada_H_Ooka_H_Hotta_I_Kojima_K_Namiki_T_Ohneda_E_Yanagi_W_Suzuki_K_Li_C_Ohtsuki_K_Shishiki_T_and_Yamamoto_M_FAI_Genome_Sequencing_Analysis_Group_Ootomo_Y_Iida_Y_Fujimura_T_Ikeda_R_Ishibiki_J_Kawamata_M_Kobayashi_M_Kodama_T_Kurosaki_T_Kusumegi_T_Lu_M_Maeda_H_Miura_J_Mizuno_K_Nakikawa_R_Nishikura_J_Oka_M_Ryu_R_Sugano_S_Yoshimura_A_Suzuki_Y_Tsunoda_Y_Ueda_M_Xie_Q_Yokomizo_S_Yoshimura_A_Matsubara_K_and_Murakami_K_Genome_Exploration_Research_Group_in_Riken_Genomic_Sciences_Center_and_Genome_Science_Laboratory_in_Riken:Adachi_J_Aizawa_K_Akimura_T_Arakawa_T_Carninci_P_Fukuda_S_Hanagaki_T_Hara_A_Hashizume_W_Hayashida_K_Hayatsu_N_Hiramoto_K_Itoha_T_Hori_F_Iida_J_Imamura_K_Imotani_K_Ishii_Y_Itoh_M_Kagawa_I_Kishikawa-Hirozane_T_Kojima_Y_Kondo_S_Kono_H_Kouda_M_Koya_S_Kurihara_C_Kurosaki_T_Kusumegi_T_Li_C_Lu_M_Maeda_H_Matsubara_K_Matsuyama_T_Miura_J_Miyazaki_A_Mizuno_K_Murakami_K_Murata_W_Nagata_T_Nakamura_M_Namiki_T_Nakikawa_R_Nishikura_J_Nishikura_M_Nomura_K_Numasaki_R_Ohneda_E_Ohno_M_Ohtsuki_K_Oka_M_Ooka_H_Ootomo_N_Ota_Y_Ootomo_Y_Ryu_R_Saitoh_H_Sakai_C_Sakai_K_Sakazume_N_Sano_H_Sasaki_D_Sato_K_Satoh_K_Shibata_K_Shinagawa_A_Shiraki_T_Shishiki_T_Sogabe_Y_Sugano_S_Sugiyama_A_Suzuki_K_Suzuki_Y_Tagami_M_Tagami-Takeda_Y_Tagawa_A_Takahashi_F_Takaku-Akahira_S_Tanaka_T_Tomaru_A_Toya_T_Tsunoda_Y_Ueda_M_Waki_K_Xie_Q_Yanagi_W_Yamada_H_Yamamoto_M_Yasunishi_A_Yazaki_J_Yokomizo_S_and_Yoshimura_A

Hirooka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ooka, H., Ooka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A., and Hayashizaki, Y.

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ORIGIN
Query Match 23.6%; Score 36.4; DB 8; Length 674;
Best Local Similarity 58.2%; Pred. No. 1.5e+03;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Oy 4 CCGAGCTGTCATTCGCTCATGTCGAGTCGCGCGCGAGCTGTCATTCGCTCAT 63
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RESULT 37
AC107207
LOCUS
DEFINITION
Oryza sativa chromosome 3 BAC OSUNBD0106M04 genomic sequence,
complete sequence.
AC107207
VERSION
AC107207.9 GI:37514985
KEYWORDS
SOURCE
ORGANISM
HNC
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehharitoidae; Oryzae; Oryza.

REFERENCE
AUTHORS
1 (bases 1 to 133449)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Gansberger, K., Jones, K.M., Overton, I., L., L., Taitlin, T., Kim, M.M., Bera, J., Jin, S., S., Fadrosch, D.W., Tallon, L.J., Koo, H., Ziemann, V., Heiao, J., Blunt, S., Vanaken, S.S., Riedmiller, S.B., Utterback, T.T., Feldlym, T.V., Yang, Q.O., Haas, B.J., Suh, B.B., Peterson, D.J., Quackenbush, J., White, O., Salzberg, S.L., and Fraser, C.M.

TITLE
Oryza sativa chromosome 3 BAC OSUNBD0106M04 genomic sequence

JOURNAL
COMMENT
Unpublished

REFERENCE
AUTHORS
2 (bases 1 to 133449)
Buell, R.

TITLE
Direct Submission

JOURNAL
Submitted (16-JAN-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REFERENCE
AUTHORS
3 (bases 1 to 133449)
Buell, R.

TITLE
Direct Submission

JOURNAL
Submitted (28-SEP-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REFERENCE
AUTHORS
4 (bases 1 to 133449)
Buell, R.

TITLE
Direct Submission

JOURNAL
Submitted (04-OCT-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA

REFERENCE
AUTHORS
5 (bases 1 to 133449)
Buell, R.

TITLE
Direct Submission

JOURNAL
Submitted (01-JAN-2004) The Institute for Genomic Research, 9712

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 repeat_region 22772..22808
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Query Match 23.6%; Score 36.4; DB 8; Length 133449;
 Best Local Similarity 58.2%; Pred. No. 5.7e+02;
 Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

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 Db 29022 CCGAGAGTCGTCGTGCGCGCGCGCGCGCGAGTCGCGAGCTGTTGCTCT 29081

Qy 64 CCGTCAGTCGCGCGCGCGCGAGTCGCGAGTCGCGAGTCGCGAGCTCG 113
 Db 29082 CATGAGCGCGCGCGCGAGAGCGAGACGCGAGCGGTCGAGCGAGCGCG 29131

RESULT 38
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 LOCUS Oryza sativa chromosome 3 BAC OSUNB0106M04 genomic sequence,
 DEFINITION complete sequence.
 AC107207 GI:37514985
 VERSION HTG.
 SOURCE Oryza sativa (japonica cultivar-group)
 KEYWORDS Oryza sativa (japonica cultivar-group)
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Euphorbiaceae; Oryzae; Oryza.
 REFERENCE 1 (bases 1 to 133449)
 AUTHORS Buell, C.R., Yuan, Q., Qiyang, S., Liu, J., Gansberger, K., Jones, K.M.,
 Overton, I.T., Taitlin, T., Kim, M.M., Bera, J.J., Jin, S.S.,
 Fadrosch, D.W., Tallon, L.J., Koo, H., Zismann, V., Heiao, J., Plunt, S.,
 Vanaken, S.S., Riedmiller, S.B., Uteback, T.T., Feldblyum, T.V.,
 Yang, Q.Q., Haas, B.J., Sun, B.B., Peterson, J.J., Quackenbush, J.,
 White, O., Salzberg, S.L. and Fraser, C.M.
 Oryza sativa chromosome 3 BAC OSUNB0106M04 genomic sequence
 Unpublished
 2 (bases 1 to 133449)
 REFERENCE Buell, R.
 TITLE Direct Submission
 AUTHORS Medical Center Dr, Rockville, MD 20850, USA
 JOURNAL Submitted (16-JAN-2002) The Institute for Genomic Research, 9712
 TITLE Medical Center Dr, Rockville, MD 20850, USA
 REFERENCE Buell, R.
 TITLE Direct Submission
 AUTHORS Medical Center Dr, Rockville, MD 20850, USA
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 REFERENCE Buell, R.
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 TITLE Medical Center Dr, Rockville, MD 20850, USA
 REFERENCE Buell, R.
 TITLE Direct Submission
 AUTHORS Medical Center Dr, Rockville, MD 20850, USA
 JOURNAL Submitted (01-JAN-2004) The Institute for Genomic Research, 9712
 TITLE Medical Center Dr, Rockville, MD 20850, USA, rbuell@igr.org
 COMMENT On Oct 4, 2003 this sequence version replaced gi:23343713.
 Address all correspondence to: rice@igr.org

BAC clone OSUNB0106M04 is from Oryza sativa chromosome 3
 The orientation of the sequence is from Sp6 to T7 end of the BAC
 clone.
 Genes were identified by a combination of several methods: Gene
 prediction programs including Fgenesh (<http://www.softberry.com/>),
 GenScan and GenScan+ (Chris Burge,
<http://CCR-081.mit.edu/GENSCAN.html>), GenMark-ES (Mark Borodovsky,
<http://genemark.biology.gatech.edu/Genemark/>), and GeneSplicer
 (Michael Pertea and Steven Salzberg, contact mpertea@tigr.org),
 searches of the complete sequence against a peptide database and
 the plant EST database at TIGR (<http://www.tigr.org/tdb/est.shtml>).
 Annotated genes are named to indicate the level of evidence for
 their annotation. Genes with similarity to other proteins are named
 after the database hits. Genes without significant peptide
 similarity but with EST similarity are named as unknown proteins.
 Genes without protein or EST similarity, that are predicted by more
 than two gene prediction programs over most of their length are
 annotated as hypothetical proteins. Genes encoding tRNAs are
 predicted by tRNAscan-SE (Sean Eddy,
<http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are
 identified by RepeatMasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSUNB0079B15 (AC099043) and
 OSUNB0072F13 (AC133450).

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repeat_region 22772..22808
/rpt_family="AT_rich"
repeat_region 22859..22954
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repeat_region 23016..23062
/rpt_family="AT_rich"

Query Match 23.6%; Score 36.4; DB 8; Length 133449;
Best Local Similarity 58.2%; Pred. No. 5.7e+02;
Matches 64; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Oy 42 CGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGCGCACTCGACGATGACGAGA 101
Db 29131 CCGGTTCCGCTACCCGCTGTCCTGCGCTCTCCGCGCGCTCGATGACGACAA 29072

Oy 102 TGACCACTCCGCGCGCGCACTGACGATGACGAGATGACCACTCCG 151
Db 29071 GCTTCGGGTGCACTCGCGTTCGCGCGCGCGCGCGCACTCCG 29022

RESULT 39
AC133450 150743 bp DNA linear PLN 31-JUN-2004
LOCUS Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence,
DEFINITION complete sequence.
ACCESSION AC133450
VERSION AC133450.6 GI:45860990
KEYWORDS HTG.
ORGANISM Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
Bacteria; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 150743)
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Gansberger,K., Jones,K.M.,
Overton II,L., Telford,T., Kim,M.M., Bera,J.J., Jin,S.S.,
Padrosh,D.W., Tallon,L.J., Koo,H., Zisman,V., Heiao,J., Blunt,S.,
Vanaken,S.S., Riedmuller,S.B., Uteback,T.T., Feldlynn,T.V.,
Yang,Q.Q., Haas,B.J., Sun,B.B., Peterson,J.J., Quackenbush,J.,
White,O., Salzberg,S.L. and Frazer,C.M.
Oryza sativa chromosome 3 BAC OSJNBa0072F13 genomic sequence
Unpublished
2 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (12-SEP-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (16-OCT-2003) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (31-MAR-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
5 (bases 1 to 150743)
Buell,R.
Direct Submission
Submitted (31-JUL-2004) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rhuel@igf.org
On Mar 31, 2004 this sequence version replaced gi:37693579.
Address all correspondence to:rice@igf.org

BAC clone OSJNBa0072F13 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
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genscan and Genescan+ (Chris Burge, <http://CCR-081.mit.edu/GENSCAN.html>), GenemarkHM (Mark Borodovsky, <http://genemark.biology.gatech.edu/Genemark/>), and Gensplizer (Mihaela Petrea and Steven Salzberg, [contact mpeete@tigr.org](http://contact.mpeete@tigr.org)), searches of the complete sequence against a peptide database and the plant EST database at TIGR (<http://www.tigr.org/tdb/tgi.shml>). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats are identified by RepeatMasker (Xian Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSUNBD0106M04 (AC107207) and OSUNBD0094O03 (AC092781).

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Best Local Similarity 60.8%; Pred. No. 1e+03;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
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Db 5323 GATCGCAGCCAGCGGACGCTTCATCGACGGAAGGGA 5359
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LOCUS DEFINITION
Bradyrhizobium japonicum isolate pMW200P9-2 putative amidase AmC
(amiC) gene, partial cds; pyruvate dehydrogenase (poxB),
2-dehydro-3-deoxyphosphogalactonate aldolase (dgok),
monooxygenase (luxA2), hpaC (hpaC), and sigma 54 activator (acor)
genes, complete cds; and unknown genes.
ACCESSION AY081837
VERSION AY081837.1 GI:20257158
KEYWORDS
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SOURCE
ORGANISM Bradyrhizobium japonicum
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE
AUTHORS Mueller, P.
TITLE TnKp2 insertions in the Bradyrhizobium japonicum poxh gene
(pyruvate dehydrogenase) affect the symbiotic interaction within
soybean nodules
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 8973)
AUTHORS Mueller, P.
TITLE Direct Submision
JOURNAL Submitted (04-MAR-2002) Biology, Cell Biology and Applied Botany,
Philipps University Marburg, Karl-von-Frisch-Str., Marburg 35032,
Germany
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GLGHVDALEPDLPRAPFEAQTKYINRPAVVISNMLARGDLDPEDLIEPMKIRI
WEAGRHISFAERAKMGVFNITSKRGAFEFQMDVILITPITALPTPKVGTREYLTISD
NPDLVDFGNLMRFPFTPLANLCGMPAISMPMATODHDPLIGIQAIAKANDGILLQ
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1586. 2179
/note="ORF197: conserved hypothetical protein"
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/db_xref="GI:20257165"
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AMSSLPYRPVPGTETGVLGVTATLDESCEMAVOLADGRIATATLDIRIDYOK
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2110. 2508
/note="ORF132"
/codon_start=1
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/db_xref="GI:20257164"
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DRRLPRDHGRTARRARRAPOADRADHQLALRPBARQLCCQDLRQAGPRIVARE
RAPGRWRTSRSPFCGHFMLRPTPGNDEE"
2579. 2842
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/transl_table=11
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FGVAFRDPERRALSTARGLALSNAPKVEPANELKALADLNGAERTITLFCGRGCA
HAPLMOLAEALKSPIVHALGKEHVEENPYDVGMTGIFGSSGGAAMHACDALVMIG
TDPPYKQFPFGCQIAQIDIRPENIGRROAHDGRSAADODPOQAQYSTMPSTTR
RARGWTRSPGAPSGSKPIHPOYLAKVSDHASEDAVPTADVGPTVAAAYVLENGR
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/product="2-dehydro-3-deoxygalactonate kinase"
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/db_xref="GI:20257161"
/translation="MSYVANDMGTSFRLMLVDRAQVLAERSGEGMLAAKTGRAG
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STFMGTGELFESVISRDTLISLAVAGADDAEDVASFKAAYAAFAFPAANLLEGASR
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TMDPDLKPHIKLPDAPHPNRVAGLSKNSDITLKEGERRGYSINLNDAAVYGSNHS
VEIGAKTGRKPRKQDMRLVREYFVADTDEEMAKLSTGMMGRMHAEITVPLIGHGF
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/db_xref="GI:20257162"
/translation="MTRRCCGAILVHPHPFRSPREVDNAKDFKQAMROCAQAVALT
GABHGKRTGLITVSACSLSDNPSSLIVCNRNASAHTRIIEBGAFAINFLHEDHALA
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ORIGIN

Query Match 23.5%; Score 36.2; DB 1; Length 8973;
Best Local Similarity 60.8%; Pred. No. 1e+03;
Matches 59; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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Db 5359 TCCCTTTCGTCGATGAGCGCTCGCTGTCGCGATCTCGCGCGCGCGAGCA 5300

Qy 79 CGCCGACTCGACGATGAGCGAGATGACCGCTCGCGC 115

Db 5299 GCGCGACTCCATCTGTCAGCGTCTGATGAGCGCGC 5263

RESULT 43
AC008771 123169 bp DNA linear PRI 28-FEB-2001

LOCUS Homo sapiens chromosome 5 clone CTD-2015H6, complete sequence.

AC008771
AC008771.4 GI:13162500

HTG.
Homo sapiens (human)

ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 123169)
DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished

2 (bases 1 to 123169)

DOE Joint Genome Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 123169)
DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

On Feb 28, 2001 this sequence version replaced gi:7709299.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.3% of Sequence;

Estimated Total Number of Errors is 0.9.

STS Content:

SHGC-84992 G53847

WI-15051 G23648

WI-17790 G24283.

Location/Qualifiers

1. 123169

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

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/clone="CTD-2015H6"

ORIGIN

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Best Local Similarity 55.0%; Pred. No. 6.3e+02;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 20 CGCTCATCTCGAGTCGCGCGCGGAGCTGATCTCGCTCATCTCGAGTCGCGCGC 79

Db 94608 CGGCGCTGTCACATGACGATCCGCTGAGGCCCAAGTAAGCGCGAGCGCGC 94667

Qy 80 GCGGACTCGACGATGAGCGAGATGACGATCTCGCGCGCGCGAGTCGAGAGAT 139

Db 94668 TCTCCCTGAGGTCGCGCGCTTTGAGAGGCTCCCGCGCGTACCTCTTTCGCGGCT 94727

Qy 140 GACGAGCTC 148

Db 94728 CCCGCGCTC 94736

RESULT 44

AC008771/c

LOCUS Homo sapiens chromosome 5 clone CTD-2015H6, complete sequence.

AC008771

AC008771.4 GI:13162500

HTG.

Homo sapiens (human)

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 123169)
DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Unpublished

2 (bases 1 to 123169)

DOE Joint Genome Institute.

Direct Submission

Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

3 (bases 1 to 123169)
DOE Joint Genome Institute and Stanford Human Genome Center.

Direct Submission

Submitted (28-FEB-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA

On Feb 28, 2001 this sequence version replaced gi:7709299.

Draft Sequence Produced by DOE Joint Genome Institute

www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center

www.shgc.stanford.edu

Quality: Phrap Quality >=40 99.3% of Sequence;

Estimated Total Number of Errors is 0.9.

STS Content:

SHGC-84992 G53847

WI-15051 G23648

WI-17790 G24283.

Location/Qualifiers

1. 123169

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="5"

/clone="CTD-2015H6"

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Query Match 23.5%; Score 36.2; DB 9; Length 123169;
Best Local Similarity 55.0%; Pred. No. 6.3e+02;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

Qy 7 GAGTGTGATCTGCTCATCTGATCGAGTCGCGCGCGGAGCTGATCTGCTCATCT 66

Db 94736 GACCGCGGAGCGCGCAAGGAGGATGAGCGCGCGGAGCTCTCAAGCGCGCACT 94677

Qy 67 CGAGTCGCGCGCGCGAGCTCGACGATGAGCGAGATGACGAGCTCCGCGCGCGAGTGA 126

ORIGIN

Db 94676 CCAGGACAGAGCGCGCGCTCGCGCTTACTTGAGGCTCCAGCGAGTGTGCATGTGA 94617
QY 127 CGATGAGCG 135
Db 94616 CGACGCCCG 94608

RESULT 45
AC018764 126052 bp DNA linear PRI 13-MAR-2003
LOCUS AC018764
DEFINITION Homo sapiens chromosome 5 clone CTD-2327L5, complete sequence.
ACCESSION AC018764
VERSION AC018764.8 GI:28933541
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 126052)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS 2 (bases 1 to 126052)
TITLE DOE Joint Genome Institute.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 126052)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (01-JUL-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 126052)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (03-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
5 (bases 1 to 126052)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (30-JAN-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
6 (bases 1 to 126052)
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
REFERENCE
AUTHORS Submitted (13-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Mar 13, 2003 this sequence version replaced gi:2814392.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.6% of Sequence;
Estimated Total Number of Errors is 0.6.
NOTE: Bacterial transposon excised at 89327.
Location/Qualifiers
1. 126052
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2327L5"

ORIGIN

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Best Local Similarity 55.0%; Pred. No. 6.2e+02;
Matches 71; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 7 GAGCTGATCATCTGCTCATCTGAGTGGGCGGAGGCTGCTCATCTGCTCATCTGT 66
Db 86827 GACCGCGGAGCCCGCAAGAGGAGGTACGCGCGGAGGCTTCAAGAGCGCCCACT 86886
QY 67 CGAGTCGGCGCGCGCACTCGACGATGAGCGAGATGACAGCTCCGCGCGCGACTCGA 126

Db 86887 CCAGGACAGAGCGCGCGCGCTCGCGCTTACTTGAGGCTCCAGCGAGTGTGCATGTGA 86946
QY 127 CGATGAGCG 135
Db 86947 CGACGCCCG 86955

Search completed: April 8, 2005, 23:58:42
Job time : 1897 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 8, 2005, 23:09:54 ; Search time 132 Seconds
(without alignments)
1908.990 Million cell updates/sec

Title: US-09-887-194A-13
Perfect score: 154
Sequence: 1 cggccgcagctgtgcacatc.....gagatgcacacgccgcgcg 154

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents, NA: *
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq: *
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq: *
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq: *
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
5: /cgn2_6/ptodata/1/ina/PTCUS_COMB.seq: *
6: /cgn2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34.8	22.6	1681	3	US-09-434-288-7 Sequence 7, Appl1
2	34.8	22.6	1681	3	US-09-434-288-7 Sequence 7, Appl1
3	34	22.1	4403765	3	US-09-103-840A-2 Sequence 2, Appl1
4	34	22.1	4403765	3	US-09-103-840A-2 Sequence 2, Appl1
5	34	22.1	4411529	3	US-09-103-840A-1 Sequence 1, Appl1
6	34	22.1	4411529	3	US-09-103-840A-1 Sequence 1, Appl1
7	33.4	21.7	747	4	US-09-252-991A-4417 Sequence 4417, Ap
8	33.4	21.7	747	4	US-09-252-991A-4417 Sequence 4417, Ap
9	33.4	21.7	3225	4	US-09-252-991A-4622 Sequence 4622, Ap
10	33.4	21.7	3225	4	US-09-252-991A-4622 Sequence 4622, Ap
11	33	21.4	345	4	US-09-513-999C-8640 Sequence 8640, Ap
12	33	21.4	345	4	US-09-513-999C-8640 Sequence 8640, Ap
13	32.4	21.0	1110	4	US-09-902-540-2360 Sequence 2360, Ap
14	32.4	21.0	1110	4	US-09-902-540-2360 Sequence 2360, Ap
15	32.4	21.0	2238	1	US-07-841-651-1 Sequence 1, Appl1
16	32.4	21.0	2238	1	US-07-841-651-1 Sequence 1, Appl1
17	32.4	21.0	15447	4	US-09-902-540-1100 Sequence 1100, Ap
18	32.4	21.0	15447	4	US-09-902-540-1100 Sequence 1100, Ap
19	32.2	20.9	579	4	US-09-252-991A-8862 Sequence 8862, Ap
20	32.2	20.9	579	4	US-09-252-991A-8862 Sequence 8862, Ap
21	32.2	20.9	807	4	US-09-252-991A-15671 Sequence 15671, A
22	32.2	20.9	807	4	US-09-252-991A-15671 Sequence 15671, A
23	32.2	20.9	876	4	US-09-252-991A-8753 Sequence 8753, Ap
24	32.2	20.9	876	4	US-09-252-991A-8753 Sequence 8753, Ap
25	32.2	20.9	1203	4	US-09-252-991A-15578 Sequence 15578, A
26	32.2	20.9	1203	4	US-09-252-991A-15578 Sequence 15578, A
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C 30	32.2	20.9	1899	4	US-09-252-991A-8973 Sequence 8973, Ap
C 31	32	20.8	921	4	US-09-902-540-3748 Sequence 3748, Ap
C 32	32	20.8	921	4	US-09-902-540-3748 Sequence 3748, Ap
C 33	32	20.8	1093	4	US-09-902-540-7905 Sequence 7905, Ap
C 34	32	20.8	1093	4	US-09-902-540-7905 Sequence 7905, Ap
C 35	32	20.8	2119	3	US-09-032-372-6 Sequence 6, Appl1
C 36	32	20.8	2119	3	US-09-032-372-6 Sequence 6, Appl1
C 37	32	20.8	7994	4	US-09-902-540-797 Sequence 797, App
C 38	32	20.8	7994	4	US-09-902-540-797 Sequence 797, App
C 39	32	20.8	17897	4	US-09-902-540-1182 Sequence 1182, Ap
C 40	32	20.8	17897	4	US-09-902-540-1182 Sequence 1182, Ap
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C 44	31.6	20.5	2622	4	US-09-252-991A-13933 Sequence 13933, A
C 45	31.6	20.5	2685	4	US-09-252-991A-13826 Sequence 13826, A
C 46	31.6	20.5	2685	4	US-09-252-991A-13826 Sequence 13826, A
C 47	31.6	20.5	34094	4	US-09-292-034-1 Sequence 1, Appl1
C 48	31.6	20.5	34094	4	US-09-292-034-1 Sequence 1, Appl1
C 49	31.4	20.4	1125	4	US-09-902-540-2467 Sequence 2467, Ap
C 50	31.4	20.4	1125	4	US-09-902-540-2467 Sequence 2467, Ap
C 51	31.4	20.4	1242	4	US-09-489-039A-3619 Sequence 3619, Ap
C 52	31.4	20.4	1242	4	US-09-489-039A-3619 Sequence 3619, Ap
C 53	31.4	20.4	1404	4	US-09-902-540-3484 Sequence 3484, Ap
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C 55	31.4	20.4	1707	4	US-09-266-965-68 Sequence 68, Appl
C 56	31.4	20.4	1707	4	US-09-266-965-68 Sequence 68, Appl
C 57	31.4	20.4	2069	4	US-09-949-016-3309 Sequence 3309, Ap
C 58	31.4	20.4	2069	4	US-09-949-016-3309 Sequence 3309, Ap
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C 60	31.4	20.4	2148	4	US-09-489-039A-3539 Sequence 3539, Ap
C 61	31.4	20.4	3202	4	US-09-949-016-1127 Sequence 1127, Ap
C 62	31.4	20.4	3202	4	US-09-949-016-1127 Sequence 1127, Ap
C 63	31.4	20.4	14077	4	US-09-902-540-1109 Sequence 1109, Ap
C 64	31.4	20.4	14077	4	US-09-902-540-1109 Sequence 1109, Ap
C 65	31.4	20.4	17188	4	US-09-902-540-1166 Sequence 1166, Ap
C 66	31.4	20.4	17188	4	US-09-902-540-1166 Sequence 1166, Ap
C 67	31.4	20.4	53500	4	US-09-266-965-76 Sequence 76, Appl
C 68	31.4	20.4	53500	4	US-09-266-965-76 Sequence 76, Appl
C 69	31.4	20.4	135667	4	US-09-949-016-15051 Sequence 15051, A
C 70	31.4	20.4	135667	4	US-09-949-016-15051 Sequence 15051, A
C 71	31	20.1	2562	4	US-09-489-039A-5900 Sequence 5900, Ap
C 72	31	20.1	2562	4	US-09-489-039A-5900 Sequence 5900, Ap
C 73	30.8	20.0	2079	4	US-09-252-991A-3097 Sequence 3097, Ap
C 74	30.8	20.0	2079	4	US-09-252-991A-3097 Sequence 3097, Ap
C 75	30.8	20.0	2787	3	US-09-105-537-40 Sequence 40, Appl
C 76	30.8	20.0	2787	3	US-09-105-537-40 Sequence 40, Appl
C 77	30.8	20.0	5970	3	US-09-320-878-21 Sequence 21, Appl
C 78	30.8	20.0	5970	3	US-09-320-878-21 Sequence 21, Appl
C 79	30.8	20.0	5970	4	US-09-141-508-11 Sequence 11, Appl
C 80	30.8	20.0	5970	4	US-09-141-508-11 Sequence 11, Appl
C 81	30.8	20.0	5970	4	US-09-141-508-11 Sequence 11, Appl
C 82	30.8	20.0	5970	4	US-09-141-508-11 Sequence 11, Appl
C 83	30.6	19.9	1734	6	US-09-657-440-21 Sequence 21, Appl
C 84	30.6	19.9	1734	6	US-09-657-440-21 Sequence 21, Appl
C 85	30.6	19.9	1734	6	US-09-657-440-21 Sequence 21, Appl
C 86	30.6	19.9	1734	6	US-09-657-440-21 Sequence 21, Appl
C 87	30.6	19.9	3114	4	US-09-902-540-1112 Sequence 1112, Ap
C 88	30.6	19.9	3114	4	US-09-902-540-1112 Sequence 1112, Ap
C 89	30.6	19.9	16833	4	US-09-902-540-8058 Sequence 8058, Ap
C 90	30.6	19.9	16833	4	US-09-902-540-8058 Sequence 8058, Ap
C 91	30.4	19.7	480	4	US-09-902-540-8058 Sequence 8058, Ap
C 92	30.4	19.7	480	4	US-09-902-540-8058 Sequence 8058, Ap
C 93	30.4	19.7	1881	4	US-09-252-991A-4030 Sequence 4030, Ap
C 94	30.4	19.7	1881	4	US-09-252-991A-4030 Sequence 4030, Ap
C 95	30.4	19.7	7160	4	US-09-902-540-821 Sequence 821, App
C 96	30.4	19.7	7160	4	US-09-902-540-821 Sequence 821, App
C 97	30.4	19.7	8563	4	US-09-902-540-3318 Sequence 3318, Ap
C 98	30.4	19.7	8563	4	US-09-902-540-3318 Sequence 3318, Ap
C 99	30.4	19.7	8604	4	US-09-902-540-5331 Sequence 5331, Ap
C 100	30.4	19.7	8604	4	US-09-902-540-5331 Sequence 5331, Ap

ALIGNMENTS

RESULT 1
US-09-434-288-7

/ Sequence 7, Application US/09434288
/ Patent No. 6303767
/ GENERAL INFORMATION:
/ APPLICANT: Betlach C., Melanie
/ TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
/ FILE REFERENCE: 30062-20030.00
/ CURRENT APPLICATION NUMBER: US/09/434,288
/ PRIOR FILING DATE: 1999-11-05
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 1681
/ TYPE: DNA
/ ORGANISM: Streptomyces narbonensis
US-09-434-288-7

Query Match 22.6%; Score 34.8; DB 3; Length 1681;
Best Local Similarity 55.9%; Pred. No. 4.6;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 1 CGGCGGAGCTGCTCATCTCGTCATCGAGTCGCGCGCGGAGCTGGTCATCTCGCT 60
DB 424 CTGGCGCGCTGCTCATCGCGGCTCACCCGCGGTCGCGCGCGGCTCGGTCGAGC 483
QY 61 CATGTCGAGTCGCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 118
DB 484 CGCGCGGAGGCGCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 541

RESULT 2

US-09-434-288-7/c
/ Sequence 7, Application US/09434288
/ Patent No. 6303767
/ GENERAL INFORMATION:
/ APPLICANT: Betlach C., Melanie
/ TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
/ FILE REFERENCE: 30062-20030.00
/ CURRENT APPLICATION NUMBER: US/09/434,288
/ PRIOR FILING DATE: 1999-11-05
/ NUMBER OF SEQ ID NOS: 12
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 7
/ LENGTH: 1681
/ TYPE: DNA
/ ORGANISM: Streptomyces narbonensis
US-09-434-288-7

Query Match 22.6%; Score 34.8; DB 3; Length 1681;
Best Local Similarity 55.9%; Pred. No. 4.6;
Matches 66; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 37 GCGCGGAGCTGCTCATCTCGTCATCGAGTCGCGCGCGGAGCTGGTCATCTCGCT 96
DB 541 GCGCGCGCGCGGAGCTGCTCATCTCGCGCTGCGCGCGGAGCTGGTCATCTCGCT 482
QY 97 CGAGATGACGAGTCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 154
DB 481 CGACCGGAGGCGCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 424

RESULT 3

US-09-103-840A-2

/ Sequence 2, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103,840A
/ PRIOR FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4403765
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ FEATURE:
/ OTHER INFORMATION: CDC 1551
/ OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 22.1%; Score 34; DB 3; Length 4403765;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 21 GTCATCTGTCGAGTCGCGCGCGGAGCTGATCTGCTCATCTCGAGTCGCGCGCGG 80
DB 4251794 GCGCGTGGCGCGCGCGGAGCTGAGACACCGCGCGCGGAGCGCGCTATC 4251853
QY 81 CGGACTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 118
DB 4251854 GCGCGGAGTCGCGCGCGGAGCTGATCTGATCTGATCTGATCTGATCTGATCT 4251891

RESULT 4

US-09-103-840A-2/c
/ Sequence 2, Application US/09103840A
/ Patent No. 6294328
/ GENERAL INFORMATION:
/ APPLICANT: FLEISCHMAN, Robert D.
/ APPLICANT: WHITE, Owen R.
/ APPLICANT: FRASER, Claire M.
/ TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
/ FILE REFERENCE: 24366-20007.00
/ CURRENT APPLICATION NUMBER: US/09/103,840A
/ PRIOR FILING DATE: 1998-06-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 4403765
/ TYPE: DNA
/ ORGANISM: Mycobacterium tuberculosis
/ FEATURE:
/ OTHER INFORMATION: CDC 1551
/ OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

Query Match 22.1%; Score 34; DB 3; Length 4403765;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 37 GCGCGGAGCTGCTCATCTCGTCATCGAGTCGCGCGCGGAGCTGGTCATCTCGCT 96
DB 541 GCGCGCGCGCGGAGCTGCTCATCTCGCGCTGCGCGCGGAGCTGGTCATCTCGCT 482
QY 97 CGAGATGACGAGTCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 154
DB 481 CGACCGGAGGCGCGCGCGCGGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTC 424

Db 4251891 GCGGTTGAGATGATCAACACCCGACTGGCCGATACGCGGCTACGCGCTGAC 4251832
Qy 97 CGAGATGACGAGCTCCGCGCCGCGACTGAGATGAGC 134
Db 4251831 CGGGGTGTCAGCTTCGCGCTTCGCGCGCCACGCGC 4251794

RESULT 5
US-09-103-840A-1

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 441529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Kv
US-09-103-840A-1

Query Match 22.1%; Score 34; DB 3; Length 441529;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 21 GCTCATGCTCGAGTCGCGCGCGGAGCTGATCTGCTCATGCTCGAGTCGCGCGCG 80
Db 4259538 GCGGTTGCGCGCCGCGCGGAGGCGAAGCTGACACCCCGCGCGGCGTACGCGCTC 4259597

Qy 81 CCGACTGACGATGAGCGAGATGACCACTCCGCGCGC 118

Db 4259598 GCGGCGAGTCGCTGCGCTGATCATCTTCAACCGC 4259635

RESULT 6
US-09-103-840A-1/c

; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 441529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Kv
US-09-103-840A-1

Query Match 22.1%; Score 34; DB 3; Length 441529;
Best Local Similarity 59.2%; Pred. No. 10;
Matches 58; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

Qy 37 GCGCGCGAGCTGATCTGCTCATGCTGAGTCGCGCGCGCGAGCTGAGCGATGAG 96
Db 4259635 GCGGTTGAGATGATCAACGCGCCGACTGCGCGGATACGCGGCTACGCGCTGCG 4259576

Qy 97 CGAGATGACGAGCTCCGCGCCGCGACTGAGATGAGC 134
Db 4259575 CGGGGTGTCAGCTTCGCGCTTCGCGCGCCACGCGC 4259538

RESULT 7
US-09-252-991A-4417

; Sequence 4417, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4417
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4417

Query Match 21.7%; Score 33.4; DB 4; Length 747;
Best Local Similarity 58.6%; Pred. No. 9.8;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 24 CATGTCGAGTCGCGCGCGGAGCTGATCTGCTCATGCTGAGTCGCGCGCGCGCG 83
Db 420 CATGTCGAGTCGCGCGCGGAGCTGATCTGCTCATGCTGAGTCGCGCGCGCGCG 479

Qy 84 ACTGACGATGAGCGAGATGACCACTCCGCGCGCGAC 122
Db 480 ACTGCTGATGCGCGCGCGAGAGCTGCTGCGCGCTTAC 518

Db

RESULT 8
US-09-252-991A-4417/c

; Sequence 4417, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4417
; LENGTH: 747
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4417

Query Match 21.7%; Score 33.4; DB 4; Length 747;
Best Local Similarity 57.0%; Pred. No. 9.8;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

Qy 33 GTGCGCGCGGAGCTGATCTGCTCATGCTGAGTCGCGCGCGCGAGCTGAGCGA 92
Db 518 GTGCGCGCGGAGCTGATCTGCTCATGCTGAGTCGCGCGCGAGCTGAGCGA 459
Qy 93 TGAAGGATGATGACGCTCCGCGCGCGAGTCAAGATGAGCGAGAT 139

Db 458 GCTGCGCACCAGCCGCTGCGCGGCTCTCTGCTGCCAGATGTCATCAT 412

RESULT 9
US-09-252-991A-4622
; Sequence 4622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4622
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4622

Query Match 21.7%; Score 33.4; DB 4; Length 3225;
Best Local Similarity 58.6%; Pred. No. 11;
Matches 58; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 24 CATTCGTCAGTGGCGCGCGGAGCTGCTATCTCGCTCATGTCGATGCGGCGCGCG 83
DB 16 CATTCGTCAGTGGCGCGCGGAGCTGCTATCTCGCTCATGTCGATGCGGCGCGCG 75
QY 84 ACTCGACGATGAGCGAGTATACCAAGTCCGCGCGCGAC 122
DB 76 ACTGCTCGATGCGCGCGCGAGCTCTGCTGCGCGCTGAC 114

RESULT 10
US-09-252-991A-4622/c
; Sequence 4622, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4622
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4622

Query Match 21.7%; Score 33.4; DB 4; Length 3225;
Best Local Similarity 57.0%; Pred. No. 11;
Matches 61; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 33 GTCGCGCGCGGAGCTGTCATCTCGCTCATGTCGATGCGCGCGCGCGACTCGACGA 92
DB 114 GTCGCGCGCGGAGCTGTCATCTCGCTCATGTCGATGCGCGCGCGCGACTCGACGA 55
QY 93 TGACGAGATGATGACGAGTCCGCGCGCGCGCGATCCAGTATGAGCGAGAT 139
DB 54 GCTGCGCAGCGCGCGCTGCGCGCGCTCTGCTGCCAGATGTCATCAT 8

RESULT 11
US-09-513-999C-8640
; Sequence 8640, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 8640
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapiens

FEATURE: NAME/KEY: misc_feature
LOCATION: 73
OTHER INFORMATION: n=a, g, c or t
FEATURE: NAME/KEY: misc_feature
LOCATION: 319
OTHER INFORMATION: y=c or t
FEATURE: NAME/KEY: misc_feature
LOCATION: 320
OTHER INFORMATION: k=g or t
FEATURE: NAME/KEY: misc_feature
LOCATION: 321
OTHER INFORMATION: y=c or t
FEATURE: NAME/KEY: misc_feature
LOCATION: 336
OTHER INFORMATION: k=g or t
FEATURE: NAME/KEY: misc_feature
LOCATION: 345
OTHER INFORMATION: m=a or c
US-09-513-999C-8640

Query Match 21.4%; Score 33; DB 4; Length 345;
Best Local Similarity 62.3%; Pred. No. 12;
Matches 48; Conservative 2; Mismatches 27; Indels 0; Gaps 0;

QY 3 GCGGAGCTGTCATCTCGCTCATGTCGATGCGCGCGCGGAGCTGTCATCTGCTCA 62
DB 246 GCGGAGCTGTCATCTCGCTCATGTCGATGCGCGCGCGGAGCTGTCATCTGCTCA 305
QY 63 TCGTCGATGCGCGCGC 79
DB 306 CCACCAGCTTACATCTC 322

RESULT 12
US-09-513-999C-8640/c
; Sequence 8640, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; PATENT NO. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24

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```

Query Match	21.4%	Score	33	DB	4	Length	345
Best Local Similarity	62.3%	Pred	No. 12				
Matches	48	Conservative	2	Mismatches	27	Indels	0
						Gaps	0

QY	76	GGCCCCCACTCGACGATAGCGAGATYACACAGCTCCGGCCGCGCACTCCACCATAGAGCG	135
	:		
Db	322	GRMRTTAGGCTGGGTGTGTGAGGAAAGACACACGTGGCGCGTAGGCTGGGTGTAGAG	253
QY	136	AGATGACCAAGCTCCGCGC	152
Db	262	AAATGACCAAGCTCGGCGC	246

```

RESULT 13
US-09-902-540-2360
: Sequence 2360, Application US/09902540
: Patent No. 6833447
: GENERAL INFORMATION:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(15849)B
: CURRENT APPLICATION NUMBER: US/09/902,540
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 60/217,883
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 16825
: SEQ ID NO 2360
: LENGTH: 1110
: TYPE: DNA
: ORGANISM: Myxococcus xanthus
US-09-902-540-2360

```

Query Match	21.0%;	Score 32.4;	DB 4;	Length 110;
Best Local Similarity	60.0%;	Pred. No. 18;		
Matches 54;	Conservative 0;	Mismatches 36;	Indels 0;	Gaps 0;

Oy	49	GATCATTCGCGCTCATCGTCAGAGTCCGGGCCCCGCACTGACGATAGCGAGATGAC	108
Db	819	GGTGGCCCGGGGCACTTTCGGCTCCACGGCGGACGAGCCATGATGGGCAAGGCACTTC	878
Oy	109	CTCCGGCCCGCGCATCTGACGATAGACGAGA	138
Db	879	CTTCGCGCGCGCATTCGGGCGTGGACCATGTA	908

```

RESULT 14
US-09-902-540-2360/C
: Sequence 2360, Application US/09902540
: Patent No. 6833447
: GENERAL INFORMATION:
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: APPLICANT: Wiegand, Roger C.
: TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
: FILE REFERENCE: 38-10(15849)B
: CURRENT APPLICATION NUMBER: US/09/902,540
: CURRENT FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: 60/217,883
: PRIOR FILING DATE: 2000-07-10
: NUMBER OF SEQ ID NOS: 16825
: SEQ ID NO 2360
: LENGTH: 1110
: TYPE: DNA
: ORGANISM: Myxococcus xanthus
US-09-902-540-2360

```

Query Match	21.0%;	Score 32.4;	DB 4;	Length 1110;
Best Local Similarity	60.0%;	Pred. No. 18;		
Matches 54; Conservative	0;	Mismatches 36;	Indels 0;	Gaps 0;

QY 17 TCTGCTCATGTCGAGTCGGGCGCGGAGTCGTGTCATCTGCTCATGTCGAGTCGGCG 76
Db 908 TCATGCTTCACGCGCATGCGCGCGCGCGAAGAGAGTGTCCTTTGCCACCATGGCTGTGCC 849
QY 77 GCCGCCGACTGCAGCATGAGCGAATGAC 106
Db 848 GCCGTGACGCGAAGGTGCGCGCGCGCACCC 819

RESULT 15
 US-07-841-651-1
 ; Sequence 1, Application US/07841651
 ; Patent No. 5410031
 ; GENERAL INFORMATION:
 ; APPLICANT: Pajor, Ana M
 ; APPLICANT: Wright, Ernest M
 ; TITLE OF INVENTION: Cloning and Functional Expression of a
 ; TITLE OF INVENTION: Mammalian Na+/Nucleoside Cotransporter: A Member of the
 ; TITLE OF INVENTION: SGLT Family
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheldon & Max
 ; STREET: 225 South Lake Avenue, Ninth Floor
 ; CITY: Pasadena
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/841,651
 ; FILING DATE: 19920224
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandel, Saralynn

; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217.883

;; PRIOR FILING DATE: 2000-07-10
;; NUMBER OF SEQ ID NOS: 16825
;; SEQ ID NO 1100
;; LENGTH: 15447
;; TYPE: DNA
;; ORGANISM: Myxococcus xanthus
US-09-902-540-1100

Query Match 21.0%; Score 32.4; DB 4; Length 15447;
Best Local Similarity 60.0%; Pred. No. 20;
Matches 54; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

Qy 49 GGTGATCTGCTCATGCTGAGTGGCGCGCGGAGCTGAGTACGATGAGTACG 108
Db 4671 GGTGCGCGCGGACCTTGGGTCCACGCGGAGCGGAGTGTGGGCAAGGCGACCTC 4612

Qy 109 CTCGCGCGCGGAGCTGAGTACGATGAGCGAGA 138
Db 4611 CTCGCGCGCGGAGCTGAGTACGATGAGCGAGA 4582

RESULT 19
US-09-252-991A-8862
; Sequence 8862, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8862
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862

Query Match 20.9%; Score 32.2; DB 4; Length 579;
Best Local Similarity 57.4%; Pred. No. 19;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 53 ATCTGCTCATGCTGAGTGGCGCGCGGAGCTGAGTACGATGAGTACGAGTCC 112
Db 280 ACCCGACCTCTACAGATATTGCTGCGCGGCAAGCGGATGCGCGAGCGACATCC 339

Qy 113 GCGCGCGAGCTGAGTACGATGAGCGAGATGACGAGTCCGCGC 153
Db 340 ATCGCGCGCAAGCGCGCGGAGGCAAGCGGAGATCATGCC 380

RESULT 20
US-09-252-991A-8862/c
; Sequence 8862, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8862

;; LENGTH: 579
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8862

Query Match 20.9%; Score 32.2; DB 4; Length 579;
Best Local Similarity 57.4%; Pred. No. 19;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 2 GCGCGAGCTGCTCATGCTGAGTGGCGCGGAGCTGAGTACGATGAGTACG 61
Db 380 GCGATGATGCTGCTGCTGCTGCGCGGCTGCGGAGTGTGATGATGCTGCGCG 321

Qy 62 ATGCTGAGTGGCGCGCGGAGCTGAGTACGAGTACGATGAGTACGAT 102
Db 320 ATCGCTTGGCGCGGAGCAATCTGATGAGTGTGCGGT 280

RESULT 21
US-09-252-991A-15671
; Sequence 15671, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15671
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15671

Query Match 20.9%; Score 32.2; DB 4; Length 807;
Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 54 TCTGCTCATGCTGAGTGGCGCGCGGAGCTGAGTACGATGAGTACGAGTCCG 113
Db 521 TCGAGCGATGCTGCGATGCTGCGGCACTGCGCGAGGCTACCGGCACTGCG 580

Qy 114 GCGCGAGCTGAGTACGATGAGCGAGATGACGAGTCCGCGCG 154
Db 581 CTGCGTACGCGAGCGCGGATTTCCGCGAGGAGTCTGCGGCTG 621

RESULT 22
US-09-252-991A-15671/c
; Sequence 15671, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15671
; LENGTH: 807
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

Query Match 20.9%; Score 32.2; DB 4; Length 876;

Query Match	20.9%	Score 32.2;	DB 4;	Length 1203;
Best Local Similarity	57.4%;	Pred. No. 20;		
Matches 58;	Conservative 0;	Mismatches 43;	Indels 0;	Gaps 0;

Qy 54 TCTGCTCATGTCGAGTCGGCGCCGCACTCGACGATGAGGAGATGACCACTCCG 113
Db 776 TCGAGCGCATGTCGCGCATGTCGCGGCACTCGCGCGGCGGCTACGCGCCCACTCGG 717
Qy 114 GCCGCCGACTCGACGATGAGGAGATGACCACTCCGCGG 154
Db 716 CTGCGGTACGCGACGCCGATTTCCGCGAGCAGCTCGGCGT 676

RESULT 27

US-09-252-991A-15737
; Sequence 15737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15737
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15737

Query Match 20.9%; Score 32.2; DB 4; Length 1869;

Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 54 TCTGCTCATGTCGAGTCGGCGCCGCACTCGACGATGAGGAGATGACCACTCCG 113
Db 1152 TCGAGCGCATGTCGCGCATGTCGCGGCACTCGCGCGGCGGCTACGCGCCCACTCGG 1211

Qy 114 GCCGCCGACTCGACGATGAGGAGATGACCACTCCGCGG 154
Db 1212 CTGCGGTACGCGACGCCGATTTCCGCGAGCAGCTCGGCGT 1252

RESULT 28

US-09-252-991A-15737/c
; Sequence 15737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15737
; LENGTH: 1869
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15737

Query Match 20.9%; Score 32.2; DB 4; Length 1869;

Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 1 CGGCCGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGCGGAGCTGTCATCTGCT 60
Db 1252 CAGCCGAGCTGTCGCGGAAATCGGCGTCCGTAACGCGAGCGGAGTTGGCGGAGGCC 1193

Qy 61 CATGTCAGTCGGCGCGCCGCACTCGACGATGAGGAGATGACCACTCCG 101
Db 1192 CTGCGCGAGTGGCGCGCATTCGCGAGCATGCGGAGTGGCTCGA 1152

RESULT 29

US-09-252-991A-8973
; Sequence 8973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8973
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8973

Query Match 20.9%; Score 32.2; DB 4; Length 1899;

Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 53 ATCTGCTCATGTCGAGTCGGCGCCGCACTCGACGATGAGGAGATGACCACTCCG 112
Db 1779 ACCCGGACCTCAACGATGTCGCGCGGCAAGCCGATCGCGGAGCATCACC 1838

Qy 113 GCCGCCGACTCGACGATGAGGAGATGACCACTCCGCGG 153
Db 1839 ATCGCGCGCAACGCCCGCGAGGCGCAAGCATGATGCT 1879

RESULT 30

US-09-252-991A-8973/c
; Sequence 8973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8973
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8973

Query Match 20.9%; Score 32.2; DB 4; Length 1899;

Best Local Similarity 57.4%; Pred. No. 20;
Matches 58; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

Qy 2 GCGCGAGCTGTCATCTGCTCATGTCGAGTCGGCGCGGCGGAGCTGTCATCTGCTC 61
Db 1879 GCGATGATCTGCCCGTTCCTCGCGCGGCGGCTGCGGCGGATGATGATGTCGCTCGCG 1820
Qy 62 ATCTGCTCATGTCGAGTCGGCGCCGCACTCGACGATGAGGAGAT 102

Db 1819 ATCGGCTTGCCGGCGCAGCAATATCTGTTGAGGTTGCGGCT 1779

RESULT 31

US-09-902-540-3748
/ Sequence 3748, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 3748
/ LENGTH: 921
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-3748

Query Match 20.8%; Score 32; DB 4; Length 921;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 48 TGTCTATCTCGCTCATCTGTCAGTGGCGCGCCGAGCTGCGATGAGCGAGATGACCA 107
DB 782 TGGGCAATCTCCACCGCGCGCGCTGTCGCGGATGAGAACTGGGCGAGATGACCG 841
QY 108 GCTCCGCGCGCGCGAGCTGCAC 127
DB 842 ACGGCAAGCGCGCTGCTCGCC 861

RESULT 32

US-09-902-540-3748/c
/ Sequence 3748, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 3748
/ LENGTH: 921
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-3748

Query Match 20.8%; Score 32; DB 4; Length 921;
Best Local Similarity 62.5%; Pred. No. 22;
Matches 50; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 28 GTTCAGTTCGGCGCGCGAGTGTATCTCGCTCATCTGTCAGTGGCGCGCGCGCACTC 87
DB 861 GGGCAGACGCGCGCTGCGCGTGCATCTGCGCCAGCTTCTGATTCACGGCGAGACAGCC 802
QY 88 GAGCATGAGCGAGATGACCA 107
DB 801 GGGCGCGGTGAGATGCCCA 782

RESULT 33

US-09-902-540-7905
/ Sequence 7905, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 7905
/ LENGTH: 1093
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-7905

Query Match 20.8%; Score 32; DB 4; Length 1093;
Best Local Similarity 53.1%; Pred. No. 22;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 27 GCTGACTCGCGCGCGAGCTGATCTGCTCATCTGTCAGTGGCGCGCGCGCACT 86
DB 281 CGCTGCGCGCTTGGCAGAGACTGAGCGTCACTCACCGGAGTGGCGAGCGCGTGTG 340
QY 87 CGACGATGAGCGAGATGACCAAGCTCCGCGCGCGCACTTCAGATGAGCGAGATGACCA 146
DB 341 CGGCGAGGCGGAGGAGCGAGCGCGCCACTGCTGCTGACAGCGCGTGTGAGAGAC 400
QY 147 TCCGCGCG 154
DB 401 TGACGCGG 408

RESULT 34

US-09-902-540-7905/c
/ Sequence 7905, Application US/09902540
/ Patent No. 6833447
/ GENERAL INFORMATION:
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 7905
/ LENGTH: 1093
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
US-09-902-540-7905

Query Match 20.8%; Score 32; DB 4; Length 1093;
Best Local Similarity 53.1%; Pred. No. 22;
Matches 68; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 CGCGCGAGCTGTATCTGCTCATCTGTCAGTGGCGCGCGAGCTGTATCTGCT 60
DB 408 CCGCTGAGCTGTGTCAGAGCGCGTGTGCAAGGCGAGGCGGCGCGCTCGCTGCGC 349
QY 61 CATCTGAGTGGCGCGCGCGCACTGCAAGATGAGCGAGATGACCACTCCGCGCGCG 120
DB 348 CTCGCGCGAGAGAGCGCGCTGCGCGAGCGCGGTGAGCTGACGCTCTGCTGCAAGC 289

QY 121 ACTGACG 128
Db 288 CCGCAGCG 281

RESULT 35

US-09-032-372-6
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032.372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;
Best Local Similarity 51.4%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 5 CGAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCTCATC 64
Db 151 CGAGCTTCTCGCTTCTCTCTCGCTCGCTCCCGCGGAAAGATGCAACGAGGGCTG 210
QY 65 GTTCAGTCGCGCGCGCGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCG 124
Db 211 CACGAGAACGAGCGCTCGCTGAAAGAGCGAGCGAGAGCTCAAGGGCAAGCTG 270
QY 125 GACGATGACGAGATGACGAGCTC 148
Db 271 GAGGAGGAGCGAGCGCAAGCTGCA 294

RESULT 36

US-09-032-372-6/c
; Sequence 6, Application US/09032372
; Patent No. 6008337
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Yue, Henry
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/032.372
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0478 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SYNORAB01
; CLONE: 78191
US-09-032-372-6

Query Match 20.8%; Score 32; DB 3; Length 2119;
Best Local Similarity 51.4%; Pred. No. 23;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

QY 7 GAGCTGTCATCTCGCTCATCTCGAGTCGCGCGCGAGCTGTCATCTCGCTCATCT 66
Db 294 GTGAGCTGTCGCTGCTCTCTCAAGCTTCCCTTGAAGCTCTCGGCTGCTTCA 235
QY 67 CGAGTCGCGCGCGCGAGCTCGAGTCGAGTCGAGTCGAGTCGAGTCGAGTCG 126
Db 234 CGAGCGCAGCTCTCTCTCTGTCGACGCCCTCGGTTCATCTTCGCGCGGAGCGAG 175
QY 127 CGATGAGGAGATGACCAAGCTCG 150
Db 174 CGAGAGGGAAGCGAGAGGCTCG 151

RESULT 37
US-09-902-540-797
; Sequence 797, Application US/0902540
; Patent No. 6833447
; GENERAL INFORMATION:

QY 28 GTCCAGTCCGCGCCGAGCTGTCATCTTCCTATCTGTCAGTCCGCGCCGCGACTC 87

Qy	Dβ
28	13468
GTCCAGTCCGCGCCGAGCTGTCATTCGCTCATCGTCGAGTCGCGCGCCGCGACTC	GGCGAGCACC GCGCTCCGTCGATATTCGCGCAGCTTCTGATTACGCGCGGACAGCGC
87	13409

QY 88 GACGATGAGCAGATGACCA 107
Db 13408 GCGCGCGGTGAGATGCCCA 13389

RESULT 41

US-09-252-991A-13526
; Sequence 13526, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13526
; LENGTH: 2496
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13526

Query Match 20.5%; Score 31.6; DB 4; Length 2496;

Best Local Similarity 62.8%; Pred. No. 29;

Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 35 GCGCGCGCGAGCTGCTCATCTGCTCATGTCGAGTCGCGCGCGCGAGCTGCGAGATG 94

Db 1013 CTGACGCGCGAGATGCGCTTCTGCTCTTGGCTTGAAGTCGCGCGCGCGAGCGATG 1072

QY 95 AGCGAGATGACCAAGCTCC 112

Db 1073 CTGATCAGATCTGTTC 1090

RESULT 42

US-09-252-991A-13526/c
; Sequence 13526, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13526
; LENGTH: 2496
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13526

Query Match 20.5%; Score 31.6; DB 4; Length 2496;

Best Local Similarity 62.8%; Pred. No. 29;

Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 43 GGAGCTGTATCTCGCTCATCTGCTCATGTCGCGCGCGCGAGCTGAGATGAGCGAGATG 102

Db 1090 GGAACAGATCTTATATGACACCGTCGCGCGCGCGCGAGCTCAAGCGAAGCGAGAA 1031

QY 103 GACCAAGCTCGCGCGCGG 120

Db 1030 GGCATCTGCGGCTGCAG 1013

RESULT 43
US-09-252-991A-13933
; Sequence 13933, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13933
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13933

Query Match 20.5%; Score 31.6; DB 4; Length 2622;

Best Local Similarity 62.8%; Pred. No. 29;

Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 43 GGAGCTGTATCTCGCTCATCTGCTCATGTCGCGCGCGCGAGCTGAGATGAGCGAGAT 102

Db 1569 GGAACAGATCTTATATGACACCGTCGCGCGCGCGCGAGCTCAAGCGAAGCGAGAA 1628

QY 103 GACCAAGCTCGCGCGCGG 120

Db 1629 GGCATCTGCGGCTGCAG 1646

RESULT 44

US-09-252-991A-13933/c
; Sequence 13933, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13933
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13933

Query Match 20.5%; Score 31.6; DB 4; Length 2622;

Best Local Similarity 62.8%; Pred. No. 29;

Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 35 GCGCGCGCGAGCTGCTCATCTGCTCATGTCGAGTCGCGCGCGCGAGCTGAGATG 94

Db 1646 CTGACGCGCGAGATGCGCTTCTGCTCTTGGCTTGAAGTCGCGCGCGCGAGCGATG 1587

QY 95 AGCGAGATGACCAAGCTCC 112

Db 1586 CTGATCAGATCTGTTC 1569

RESULT 45

US-09-252-991A-13826
; Sequence 13826, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13826
; LENGTH: 2685
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13826

Query Match 20.5%; Score 31.6; DB 4; Length 2685;
Best Local Similarity 62.8%; Pred. No. 29;
Matches 49; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 43 GGAGCTGGTCACTCTGCTCATGCTGAGTGGGCGCGCCGCCGACTCGACGATGAGGAGAT 102
DB 1576 GGAACAGATCCGATCAGCAGCAGCGTGGGCGCGCCGCCGACTCGACGATGAGGAGAT 1635
QY 103 GACCAGCTCCGGCCCGG 120
DB 1636 GGCCTATCTGCGCTGTCAG 1653

Search completed: April 9, 2005, 00:55:08
Job time : 154 secs